Attachment I

	Usizy/ nomo sapien				:	1681
	Omo			1.0	117 5	1490
	homo sap			7.6	•	8
	drosophi			7.6	•	8
RP NUCLEOTIDE SEQUENCE [LARGE &	troglo	1 SIGL1_PANTR	597 1	7.6	117.5	8
	homo	-		7.6	٠	1486
	DOM I			7.6	•	æ
				7.6	17	8
				7.6	7	9
		-		7.0		1487
		2 Q59EJ9_HUMAN		1.0	٠	1480
	mod.			7.6	٠	٠.
	caeno			7.6	μ	1478
				7.6	118	1477
	homo	•		7.6		1476
	omod			7.6	118	1475
	Q8n475 homo sapien	TLS	847	7.6	118	1474
	Domo	NAMON / NAMED	838	•	: =	1473
	xeno	Z QYIBY XENIA	ο μ φ		: :	7/11
	Omon	POTAS HOPEN	000	٠.	: -	1/17
	Barrns dar	CENT CHICK	000		: :	777
				7:0	:;	1470
	אלנוטקטיוס או			7 :	<u> </u>	1469
	Yenonue 1s			7.6	<u>-</u>	1468
	1007	O4RV46 TRTNG		7 6		1467
	callus ca				=	1466
	cotur			7.6	=	1465
	homo			7.6	Ľ	1464
	homo			7.6	118	1463
	Q9nt99 homo sapien			7.6	118	1462
	tetra			7.6	118	1461
	Q4sda6 tetraodon n			7.6	118	1460
	anopheles			7.6	PIT	1459
	nomo sapie			•	118	1400
	anopneres			1.	110	140/
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	Contact Carlos			7 .	<b>⊸</b> j	1454
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	OAtovo tetrandon n			7		1452
TOUTHOUTHOUT OUGODING THE TOUTHOUTH THE TOUTH THE	OAsins tetracion n		2646	7 7	118.5	1451
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	Ostins anonheles of			7.7	118.5	1448
	OBWT45 Caenorhabdi	-		7.7	90 (	4
		-		7.7	Θ.	1446
	anoph			7.7		1445
				7.7		1444
	rat	2 OGIRHS RAT		7.7		4
				7.7	œ	4
	drosc	2 Q9VCT4 DROME	545	7.7	18.	1441
	homo	2 Q8NOZ9 HUMAN	540	7.7	8	A
DT 13-SEP-2005 (Rel. 48, Last		2 Q9NWQ7 HUMAN	538	7.7	•	1439
	dros	2 P91670 DROME	528	7.7	8	1438
		1 SIGL7 HUMAN	467	7.7	8	1437
	≅	2 QBBFX8 MOUSE	397	7.7	•	1436
ID JAM1 HUMAN STANDARD:		O8BLX5		7.7	118.5	1435
JAM1 HUMAN	_	076697		7.7	8	1434
RESULT 1	rattu	P97635		7.7	Φ.	1433
	ovis aries	OSYJIO		7.7	80	1432
	Sanna brachv	OSSNN8 BRA		7.7	•	1431
	DOD .	OSRC22 PONP	69	7.7	8	1430
	8k1h8	8HTX80	63	7.7	œ	1429
	Sbi91 drosop	05815	90	7.7	119	1428
117.5 7.6 6710	O9vn14 drosophila	CONT DR		7.7	119	1427
117.5 7.6 2343	589q5 qallus	058965	87	7.7	119	1426
117.5 7.6 1251	B drosophila	07KP08	80	7.7	119	1425
117.5 7.6 1240	tetraodon	048504	75	7.7	119	1424
117.5 7.6 1198	481C0	04810	20	7.7	119	1423
117.5 7.6 1089	Q80y42 mus musculu	Q80Y42	-	7.7	-	1422
117.5 7.6 848	86CV9	O86CY9-	22	7.7	⊷	1421
1493 117.5 7.6 793 2	0699p0 antheraea p	2 Q699PO ANTPE	413	7.7	119	1420
117.5 7.6 764	Q8isf5 caenorhabdi	Q8ISF5	_	7.7	119.5	1419

## ALIGNMENTS

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RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Touchman J.W., Green S.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green S.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT and mouse cDNA sequences.";
and mouse cDNA sequences.";
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                                                                                                                                                                                                                                                                                                                                            INTERACTION WITH MPDZ.

PubMed=11489913; DOI=10.1083/jcb.200103047;

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Itoh M., Sasaki H., Furuse M., Ozaki H., Kita T., Tsukita "Junctional adhesion molecule (JAM) binds to PAR-3: a poss mechanism for the recruitment of PAR-3 to tight junctions.
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PubMed=15340161; DOI=10.1110/ps.04682504;
Zhang Z., Henzel W.J.;
"Signal peptide prediction based on analy:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAIK U.P., Ehrlich Y.H., Kornecki B.;
"Mechanisms of platelet activation by
linking of a novel platelet receptor f
the FC gamma RII receptor.";
Biochem T Tire-T-
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Trends
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Thomas G.R., Vandekerckhove J.;
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Gevaert K., Goethals M., Martens L., Van Damme J., Sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=7646439
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                                "Leukocyte-endothelial-cell interactions in leukocyte transmigration and the inflammatory response.";
Trends Immunol 24:327-334(2003)
                                                                                                                                                        Muller W.A.;
                                                                                                                                                                                                 PubMed=12810109;
FUNCTION:
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                                                                                                                                                                                                                                                                                                            Biol. 154:491-497(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. 310:155-162(1995).
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                                                                                                                                                                                                                                      NOMENCLATURE
    Seems
                                                                                                                                                                                                 DOI=10.1016/S1471-4906(03)00117-0;
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for monoclonal antibody F11 with
        epithelial tight junction
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junctions.";
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PDB; 1NBQ; X-ray; A/B=27-233
Ensembl; ENSG00000158769; Hor
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between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
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                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                            3D-structure; Direct protein sequencing; Glycoprotein; Immunoglobulin domain; Repeat; Signal; Tight junction; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; 1.
PROSITE; PS50835; IG_LIKE; 2.
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                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          formation. Appears early in primordial forms of cell junctions recruits PARD3. The association of the PARD6-PARD3 complex may prevent the interaction of PARD3 with JAM1, thereby preventing tight junction assembly (By similarity). Plays a role in regulating monocyte transmigration involved in integrity of epithelial barrier. Involved in Platelet activation.

SUBUNIT: Interacts with the first PDZ domain of PARD3. The association between PARD3 and PARD6B probably disrupts this interaction (By similarity). Interacts with the ninth PDZ domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO:0005911; C:intercellular junction; TAS
GO:0006954; P:inflammatory response; TAS.
erPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: N-Glycosylated.
SIMILARITY: Belongs to the immunoglobulin superfamily.
SIMILARITY: Contains 2 Ig-like V-type (immunoglobulin-like)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type I membrane protein (Potential).
Localized at tight junctions of both epithelial and endothelial
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                            181
                                                                               121
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                  RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240
                                                                                                         EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYG
                                                                                                                        EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYG 120
                                                                                                                                                             RAPSNSSYVLNPTTGELVPDPLBASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV
                                                     EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEODGSPPSE
                                                                    EVKVKLIVLVÞÞSKÞTVNIÞSSATIGNRAVLTCSBQDGSÞÞSEYTWFKDGIVMÞTNÞKST 180
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NUMBLICE (MAY-2005) to the EMBL/GenBank/DDBJ RMBL; CR533512; CAG38543.1; -; mENA.

MBL; AF191495; AAG28379.1; -; mENA.

MBL; AF490407; AAG284756.1; -; Genomic_DNA.

MBL; BT020103; AAV38906.1; -; mENA.

MBL; AL591806; CAL15365.1; -; Genomic_DNA.

MBL; AK075152; BAC11436.1; -; mRNA.

MR; Q6F1B4; 25-233.
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34 HUMAN
QEFIB4 HUMAN PRELIMINARY;
QEFIB4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Isogai T.;
"Signal Sequence and Keyword Trap in silico for Selection of Full-
Length Human cDNAs Encoding Secretion or Membrane Proteins from Ol-
Tapped cDNA Libraries.";
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MEDLINE-20537956; PubMed=11087121; DOI=10.1080/15216540050176593;
Gupta S.K., Pillarisetti K., Ohlstein B.H.;
"Platelet agonist F11 receptor is a member of the immunoglobulin superfamily and identical with junctional adhesion molecule (JAM):
                                                                                                                                                                                                                                                                                                                                                                                                  Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Phelan M., Farmer A.; "Cloning of human full-length CDSs in BD Creator(TM) System
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kalnine N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Identification and characterization of KAT, a novel gene preferentially expressed in several human cancer cell lines.", Biol. Chem. 384:763-775(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22701983; PubMed=12817473; DOI=10.1515/BC.2003.085; Wenzel K., Felix S.B., Flachmeier C., Heere P., Schulze W., Grunewald I., Pankow H., Hewelt A., Scherneck S., Bauer D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLECTIDE SEQUENCE.

Rebert L., Schick M., Neubert P., Schatten R., Henze S., Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                         Barrison B
                                                                                                                                                                                                                                                                                  WCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                               submitted (OCT-2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       regulation of expression in human endothelial cells and macrophages.", IUBMB Life 50:51-56(2000).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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Baer J., Lin
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RESULT 3
Q9Y5B2 II
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AC Q9Y5
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Matches 299;
                             Query Match
Best Local
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GO; GO:0004872; F:receptor activity; IRA.
InterPro; IPR003599; IG.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR007110; Ig-2.
InterPro; IPR003598; Ig-c2.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; IG; 1.
SMART; SM00409; IG; 2.
SMART; SM00406; IGC2; 2.
SMART; SM00406; IGC2; 2.
SMART; SM00406; IGC2; 1.
PROSITE; PS50835; IG-LIKE; 2.
                                                                                                         PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin domain; Transmembrane
SEQUENCE 259 AA; 28122 MW; FE385;
                                                                                                                                                                                                                                                                                                                                                       Liu Y., Nusrat A., Schnell F.J., Walsh S., Rea Poley C., Parkos C.A.; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ-i-SUBCELLULAR LOCATION: Type I membrane prot EMBL; AF154005; AAD43794.1; -; mRNA.
                                                                                                                                                                               Ensembl; ENSG00000158769; Homo InterPro; IPR007110; Ig-like. InterPro; IPR003598; Ig-c2. Pfam; PF00047; Ig; 2. SMART; SM00408; IGc2; 1.
                                                                                                                                                                                                                                                                                                                 HSSP; Q9Y624; INBQ.
SMR; Q9Y5B2; 20-193
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
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Q9Y5B2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Junction adhesion molecule.
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     al Similarity
257, Conserv
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Score 1281; DB 2;
Pred. No. 3.8e-91;
0; Mismatches 2;
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Matches

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JAM1 RÖT
Q8VC39 MOUSE
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Q699P0_ANTPE
Q86CY9_HELAM
Q80CY42_MOUSE
Q4S1C0_TETING
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Name=FilR; Synonyms=JAM1, J
Homo sapiens (Human).

Eukaryota; Metazoa; Chordat
Mammalia; Eutheria; Euarcho
    NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

MEDILINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

MEDILINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

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MEDLINE=99323940; PubMed=10395639;

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Q4RY64_TETING
Q25198_HYDAT
PGFRA_HUMAN
Q60T65_CAEBR
NFASC_MOUSE
Q62D54_MOUSE
Q5TX11_ANOGA
Q61SF4_CAEBR
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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.K.,
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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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mechanism for the recruitment of PAR-3 to tight junctions.";
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Gevaert K., Goethals M., Martens L., Van Damme J., Sta
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PubMed=15340161; DOI=10.1
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                                                                      "Leukocyte-endothelial-cell interactions
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                                                                                                                                   AND
                                               inflammatory
                                                                                                                                                                      Biol. 154:491-497(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     340161; DOI=10.1110/ps.04682504;
Henzel W.J.;
                                                                                                                                 NOMENCLATURE
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                                                                                                             DOI=10.1016/S1471-4906(03)00117-0;
                                                                                                                                                                                                                                                                                                               21:566-569(2003).
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                                                   response
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              plays a role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kornecki E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCALE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a stimulatory
            epithelial tight junction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND N-GLYCOSYLATION
                                                                      ín
                                                                      leukocyte transmigration
                                                                                                                                                                                                                                                                                                                                                                                             Staes
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antibody F11 with
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM;
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EMBL; BC001533; AAH
PIR; A59406; S56749
                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005911; C:intercellular GO; GO:0006954; P:inflammatory r
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                                                                                                                                                                                                                                                                                  DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ensembl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This Swiss-Prot
                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50835;
                                                                                                                                                                                                                                                                                                                                                                      mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                    D-structure; Direct
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e as long a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              formation. Appears early in primordial forms of cell junctions recruits PARD3. The association of the PARD6-PARD3 complex may prevent the interaction of PARD3 with JAM1, thereby preventing tight junction assembly (By similarity). Plays a role in regulating monocyte transmigration involved in integrity of epithelial barrier. Involved in platelet activation.

SUBUNIT: Interacts with the first PDZ domain of PARD3. The association between PARD3 and PARD6B probably disrupts this interaction (By similarity). Interacts with the ninth PDZ domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTM: N-Glycosylated.
SIMILARITY: Belongs
SIMILARITY: Contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of MPDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1NBQ; X-ray; A/B=27-233
mbl; ENSG00000158769; Hou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Localized
       181
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AL136649;
                                                                                                                                                                                 299;
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AF207907;
                                                                                 61
                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  wiss-Prot entry is copyright. It is produced through a collaboration n the Swiss Institute of Bioinformatics and the EMBL outstation - ropean Bioinformatics Institute. There are no restrictions on its long as its content is in no way modified and this statement is not
                                                                                                                                                                                              Similarity
                                                                                                                                               MGTKAQVERKILCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV
RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV
                                 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST
                                                EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST
                                                                               EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYG
                                                                                                         EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYG
                                                                                                                                                                                                                                                                                                                                                                                                                       IPR007110;
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239
260
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                                                                                                                                                                                                                                                                                                                                                                       domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Belongs to
Contains 2
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                                                                                                                                                                                                                                                        100.0%;
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                                                                                                                                  LCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV
                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                              LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                    Ig-like
                                                                                                                                                                                                                                                                                                                                                                       Repeat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the immunoglobulin superfamily. Ig-like V-type (immunoglobulin-like)
                                                                                                                                                                                 <u>.</u>
                                                                                                                                                                                                                                                                 Extracellular (Potential).
Potential.
Cytoplasmic (Potential).
Ig-like V-type 1.
Ig-like V-type 2.
Ig-like V-type 2.
Ig-like (GlcNAG. . . .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                      sequencing; Glycoprotein;
;; Signal; Tight junction;
                                                                                                                                                                                                                                               Potential.
                                                                                                                                                                                                                                                          Potentia.
                                                                                                                                                                                                                                                                                                                                             Junctional adhesion molecule
                                                                                                                                                                                             Score 1544; DB 1;
Pred. No. 1.8e-111;
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mRNA.
mRNA.
mRNA.
mRNA.
mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  response;
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                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              membrane protein (Potential).
of both epithelial and endothelial
                                                                                                                                                                                                                                                                                                                                                                      junction; Transmembrane
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                                                                                                                                                                                   Indels
                                                                                                                                                                                                          Length
                                                                                                                                                                                                           299;
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RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV

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RESULT OF SECTION OF S
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                      Submitted (MAY-2005) to the EMBL RMBL; CR533512; CAG38543.1; -; m EMBL; AF191495; AAG2879.1; -; m EMBL; AF490407; AAO84556.1; -; G EMBL; BT020103; AAV38906.1; -; m EMBL; AK951806; CA115365.1; -; c EMBL; AK075152; BAC11436.1; -; m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q6FIB4
                                                                                                                                                                                                                                                                                          Phelan M., Farmer "Cloning of human vector.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length Human cDNAs Encoding Capped cDNA Libraries."; DNA Res. 12:117-126(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Otsuki T., Ota T., Nishikawa T., Hayashi K., Suzuki Y., Yamamoto J. Wakamatsu A., Kimura K., Sakamoto K., Hatano N., Kawai Y., Ishii S. Saito K., Kojima S., Sugiyama T., Ono T., Okano K., Yoshikawa Y., Saotsuka S., Sasaki N., Hattori A., Okumura K., Nagai K., Sugano S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
MEDLINE=22701983; PubMed-
Wenzel K., Felix S.B., Fl
Grunewald I., Pankow H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20537956; PubMed=11087121; DOI=10.1080/15216540050176593; Gupta S.K., Pillarisetti K., Ohlstein E.H.; "Platelet agonist F11 receptor is a "Platelet agonist F11 receptor is superfamily and identical with junctional adhesion molecule (JAM): regulation of expression in human endothelial cells and macrophages."; TUBMB Life 50:51-56(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
Ebert L., Schick M.,
Submitted (JUN-2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
FIR protein (Fil receptor protein) (JAMI) (Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preferentially expressed in s
Biol. Chem. 384:763-775(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                      Submitted
                                                                                                                                                                                                                                                                                                                                                            Kalnine N., Chen X., Rolfs
Koundinya M., Raphael J., M
                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=F11R; ORFNames=RP11-544M22.2-001;
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                                                                                                                                                                                               Harrison E.
                                                                                                                                                                                                                           NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification and characterization of KAT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
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     Q6FIB4;
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                                                                                                                                                                                                                                                                      (OCT-2004)
                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Human)
                                                                                                                                                                                                                                                                                                               A.;
full-length CDSs in
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3.B., Flachmeier C., Heere P., Schulze W.,
cow H., Hewelt A., Scherneck S., Bauer D.,
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Moreira D., Kell
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                         Genomic_DNA mRNA.
                                                                         Genomic_DNA.mRNA.
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Kelley T., I
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                                                                                                                                                                                                                                                                                                                    Creator (TM)
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Catarrhini; Hominidae;
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aer J., Lin
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PRESULT

Q975B2

ID Y5B2

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AC Q9

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Best Local (
Matches 257;
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EMBL; AF154005; AAD43794.1; -; mRNA.
HSSP; Q9Y624; INBQ.
SMR; Q9Y582; 20-193.
Ensembl; ENSG00000158769; Homo sapiens.
InterPro; IPR007310; Ig-11ke.
InterPro; IPR0073598; Ig-2:
SMART; SM00408; IGC2; 1.
PROSITE; PS50835; IGC2; 1.
PROSITE; PS50835; IGC2; 1.
PROSITE; PS50835; IGC2; 1.
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InterPro; IPR007110; Ig-1ike.
InterPro; IPR007110; Ig-c2.
InterPro; IPR003598; Ig-v.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; Ig; 1.
SMART; SM00409; IG; 2.
SMART; SM00408; IGc2; 2.
SMART; SM00408; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 22, 101-OCT-2003 (TrEMBLrel. 25, 17) Unction adhesion molecule.

Homo sapiens (Human).

Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Euarchont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                       Liu Y., NuBrat A., Schnell F.J., Walsh S., Kedves I.A., Foley C., Parkos C.A.; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9Y5B2_HUMAN
Q9Y5B2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003599;
InterPro; IPR007110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN
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                                                                                         28122 MW;
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Last annotation updat
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                       Score 1281;
Pred. No. 3
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Pred. No. 1.8e-11
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Mismatches
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MEDLINE=99323940; PubMo
Ozaki H., Ishii K., Hoo
Iwamatsu A., Kita T.;
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Q9XT56;
16-OCT-2001
16-OCT-2001
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13-SEP-2005 (Rel. 48, Last ar
Junctional adhesion molecule
molecule 1) (JAM).
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Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Combined treatment of TNF-alpha and IFN-gamma causes redistribution of junctional adhesion molecule in human endothelial cells.";
J. Immunol. 163:553-557(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=F11R; Synonyms=JAM1;
                                                                                                                                                                                                      between
                                                                                                                                                                                                                                This Swiss-Prot entry is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pecora; Bovidae;
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                                                                                                                                                    European
as long a
                                                                                                                                                                                                                                                                                                                                                               similarity).
SUBCELLULAR LOCATION: Type I membrane racalized at tight junctions of both (
                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Seems to plays a role in epithelial tight junction formation. Appears early in primordial forms of cell junctions recruits PARD3. The association of the PARD6-PARD3 complex may prevent the interaction of PARD3 with JAM1, thereby preventing tight junction assembly (By similarity). Plays a role in regulating monocyte transmigration involved in integrity of epithelial barrier. Involved in platelet activation. SUBUNIT: Interacts with the first PDZ domain of PARD3. The association between PARD3 and PARD6B probably disrupts this interaction. Interacts with the ninth PDZ domain of MPDZ (By interaction). Interacts with the ninth PDZ domain of MPDZ (By
                                                                                                                                                                                                                                                                                                    Localized at tight ju
cells (By similarity)
SIMILARITY: Belongs t
SIMILARITY: Contains
                    ; Q9Y624; 1NBQ.
Q9XT56; 24-232
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                                                                           AF111714; AAD42051.1;
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                                                                                                                                                                         rot entry is copyright. It is produced through Swiss Institute of Bioinformatics and the EN Bioinformatics Institute. There are no resti
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neria; Cetartiodactyla;
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(immunoglobulin-like)
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; Ruminantia;
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RESULT QSEVER PRESULT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
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SMART; SM00408; IGc2; 1.
PROSITE; PS50835; IG_LIKE; 2.
Glycoprotein; Immunoglobulin
                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
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10-MAY-2005 (TrEMBLrel.
10-MAY-2005 (TrEMBLrel.
F11 receptor isoform a.
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Q5E9V8;
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                     NUCLEOTIDE SEC
                                                                                                                                                       Heaton M.P., Lac
Pertea G., Holt
                                                                                                                                                                                                                 Smith
                                                                                                                                                                                                                                   MEDLINE=21180013; PubMed=11282978; DOI=10.1101/gr.170101;
                                                                                                                                                                                                                                                     TISSUE-Pool
                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus
                                                                           "Sequence evaluation of four poolibraries and construction of a Genome Res. 11:626-630(2001).
                                                                                                                                       Keele J.W.;
                                                                                                                                                                                               Савав Е.,
                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9913;
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                                                                                                                                                   T.P.L., Grosse W.M., Freking B.A., Roberts A.J., E., Wray J.E., White J., Cho J., Fahrenkrug S.C., n M.P., Laegreid W.W., Rohrer G.A., Chitko-McKown a G., Holt I., Karamycheva S., Liang F., Quackenbu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYG
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                                       SEQUENCE
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5 (TrEMBLrel. 30,
5 (TrEMBLrel. 30,
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 Sonstegard
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74.6%;
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Cytoplasmic (Potential Ig-like V-type 1.
Ig-like V-type 2.
N-linked (GlcNAc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
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                                                                                                 pooled-tissue
f a gene index
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Pred. No. 5.6e
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Junctional adhesion molecu
Extracellular (Potential).
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     Clawson
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                                                                                             gene
   М.
Г.
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                                                                                                                                                                           Roberts A.J., Stone ahrenkrug S.C., Benne Chitko-McKown C.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; DB 1; Length .6e-83;
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                                                                                                 normalized for cattle.
     Heaton
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                                                                                                                                                         Quackenbush
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC64;
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                                                                                                   bovine .";
                                                                                                                                                                             Bennett
C.G.,
       Keele
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                                                                                                                                                                                               R.T.,
     J.₩.,
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Best Local
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Q9JHY1;
13-SEP-2005 (Rel. 48, 1
13-SEP-2005 (Rel. 48, 1
13-SEP-2005 (Rel. 48, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequencing clones."; Submitted (F
                                                                                                                                                                                                                                                                                                         STRAIN=Sprague-Dawley;
Mashima H., Kojima I.;
Submitted (JUN-2000) to
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                      TISSUE-Prostate;
NIH - Mammalian Gene Collection (MGC) project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Junctional adhesion molecule A precursor (JAM-A) (Junctional adhesion molecule 1) (JAM).
                                                                                                                                                                                                                               Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=F11r; Synonyms=Jam1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (FEB-2005) to the EMBL/Ger EMBL; BT020812; AAX08829.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Snelling
   ÷
                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [MRNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match
                                                                      FUNCTION: Seems to play a role in epithelial tight junction formation. Appears early in primordial forms of cell junctions recruits PARD3. The association of the PARD6-PARD3 complex may prevent the interaction of PARD3 with JAM1, thereby preventing tight junction assembly. Plays a role in regulating monocyte transmigration involved in integrity of epithelial barrier. Involved in platelet activation (By similarity). The association between PARD3 and PARD6B probably disrupts this interaction. Interacts with the first PDZ domain of PARD3. The association. Interacts with the first PDZ domain of MPDZ (By interaction. Interacts with the first PDZ domain of MPDZ (By
                                           interaction. Interacts with similarity).
SUBCELLULAR LOCATION: Type
               Localized at tight jucells (By similarity)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W.M., Weidmann R.T., Smith T.P.L.; ing and analysis of Bos taurus full-length insert
N-Glycosylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV
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74.6%;
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Last annotation update)
                               junctions
 (By similarity)
                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ
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Pred. No. 5.6
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QBVC39;

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EMBL; BC065309; AAH65309.1; -;
HSSP; O88792; 1F97.
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SIGNAL
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InterPro; IPR003596;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVSIHLTVLVPPSKPTVSIPSSVTIGNRAVLTCSEHDGSPPSEYSWFKDGVPMLTADAKK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPT-NPKS
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Immunoglobulin
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Extracellular (Potential).
Potential.
Cytoplasmic (Potential).
Ig-like V-type 1.
Ig-like V-type 2.
N-linked (GlcNAc. ..) (Pote
By similarity.
By similarity.
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Pred. No. 9e-77;
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NUCLEOTIDE SEQUENCES

RY
STRAIN=C57BL/6J; TISSUB=Cecum;
RC
STRAIN=C57BL/6J; TISSUB=Cecum;
RX
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RX
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RX
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RX
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RX
MEDLINE=21085660; PubMed=11217851; Coshino M., Itoh M., Ishi Y.,
RA
Kawai J., Shinagawa A., Shibata K., Konno M., Kondo S., Yamanaka I.,
RA
Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,
RA
Fleischmann W., Gassterland T., Gissi C., King B., Kochiwa H.,
RA
Fleischmann W., Gassterland T., Gissi C., King B., Kochiwa H.,
RA
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA
Suzuki H., Toyo-oka K., Wang K.H., Westz C., Whittaker C., Wilming L.,
RA
Suzuki H., Toyo-oka K., Wang K.H., Westz C., Whittaker C., Wilming L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Manmary tumor. WAP-TGF alpha model. 7 months old;

RX MEDLINE=22388257; pubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=22388257; pubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., William R.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length human

"Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA secuences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Buarchontoglires; Glires, Rodentia, Sciurognal Muroidea, Muridae, Muridae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Mix FVB/N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Mix FVB/N;
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er J., Wiemann
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Cecum;
MEDINB=20530913; PubMed=1107861; DOI=10.1101/gr.152600;
MEDINB=20530913; PubMed=11078661; DOI=10.1101/gr.152600;
Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaghazama M., Nishine T., Kashiwagi K.,
Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Yokazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II
"Analysis of the mouse transcriptome based on functional
60,770 full-length CDNAs "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs t prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10:1617-1630(2000).
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[7]
                                                                                                             Pfam; PF00047; ig; 1.
SMART; SM00406; IGV;
                                                                                                                                                                                                                                                                            HSSP; 088792; 1P97.
SMR; Q8VC39; 27-238.
Ensembl; ENSMUSG00000038235; Mus musculus
                                                                                                                                                                                                                                                                                                                                     EMBL; BC021876; AAH21876.1; -; mRNA.
EMBL; CT010347; CAJ18555.1; -; mRNA.
EMBL; AK033574; BAC28369.1; -; mRNA.
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                                                                                                                                                     InterPro;
                                                                                                                                                                  GO:0005923; C:tight junction; IDA.
GO:0005915; F:protein binding; IPI.
GO:0007155; P:cell adhesion; IDA.
GO:0030855; P:celthelial cell differentiation; IDA
erPro; IPR007110; Ig-like.
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   Similarity
                                                                            lobulin
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                                                         300 AA;
                                                                                             IG_LIKE;
   69.9%;
                                                         32424 MW;
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   Score 1079.5;
Pred. No. 1.96
                                                           3CE561E8FF3B97EC CRC64;
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.5; DB 2;
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Matches

Conservative

44;

48;

Indels

3,

Gaps

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JAM1 MO
088792;
                                                                                                                         MEDIINE=21340266; PubMed=11447115; DOI=10.1093/emboj/20.14.3738; Ebnet K., Suzuki A., Horikoshi Y., Hirose T., Meyer zu Brickwedde M.-K., Ohno S., Vestweber D.; "The cell polarity protein ASTB/PAR-3 directly associates with junctional adhesion molecule (JAM)."; EMBO J. 20:3738-3748(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                          MUCLEOTIDE SEQUENCE.

MEDLINE=98327120; PubMed=9660867; DOI=10.1083/jcb.142.1.117;

Martin-Padura I., Lostaglio S., Schneemann M., Williams L., Romano

Martin-Padura I., Lostaglio S., Schneemann M., Williams A., Romano

Panzeri C., Stoppacciaro A., Ruco L., Villa A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=Fllr; Synonyms=Jaml, Jcam, Jcaml;
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata;
Mammalla; Butheria; Euarchontoglires; Gl
Mamroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation updat
Junctional adhesion molecule A precursor (J
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Pruscella P., Pan...
Prosion m
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Winkler F.K., Hennig M.;
"X-ray structure of junctional adhesion homophilic adhesion via a novel dimeriza EMBO J. 20:4391-4398(2001)
                                                    X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 212-238.
MEDLINE=21391702; PubMed=11500366; DOI=10.1093/emboj/20.16.4391;
Kostrewa D., Brockhaus M., D'Arcy A., Dale G.E., Nelboeck P.,
Schmid G., Mueller F., Bazzoni G., Dejana E., Bartfai T.,
                                                                                                                                                                                                       INTERACTION WITH PARD3.
MEDLINE=21340266; PubMe
                                                                                                                                                                                                                                                                    MEDLINE=20489356; PubMed=11036763; Aurrand-Lions M.A., Duncan L., Du Pasquier L., Imhof "Cloning of JAM-2 and JAM-3: an emerging junctional affamily?";
                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION.
                                                                                                                                                                                                                                                                                                                                                                   monocyte transmigration."
                                                                                                                                                                                                                                                                                                                                                                                 "Junctional adhesion molecule, a novel member of the immunoglobulin superfamily that distributes at intercellular junctions and modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             molecule 1) (JAM).
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Rodentia; Sciurogna
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[5]
REVIEW, AND NOMENCI
MEDLINE=22695901; E
Muller W.A.;
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EMBL; U89915; AAC32982.1; -; PDB; 1F97; X-ray; A=27-238. Ensembl; ENSMUSG00000038235;
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SIMILARITY: 0
domains.
                                                                                                                                                                                                                                                                                                            interaction.
SUBCELLULAR LOCATION: Type I membrane rocalized at tight junctions of both 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nds Immunol. 24:327-334(2003).

FUNCTION: Seems to plays a role in epithelial tight junction formation. Appears early in primordial forms of cell junctions recruits PARD3. The association of the PARD6-PARD3 complex may prevent the interaction of PARD3 with JAM1, thereby preventing tight junction assembly. Plays a role in regulating monocyte transmigration involved in integrity of epithelial barrier.
                                                                                                                  as
                                                                                                                                                                                                                                                                                                                                                                                               Involved in platelet activation.
SUBUNIT: Interacts with the ninth PDZ domain of MPDZ (By similarity). Interacts with the first PDZ domain of PARD3.
association between PARD3 and PARD6B probably disrupts thi
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Swiss Institute of Bioinformatics and the EMBL
Bioinformatics Institute. There are no restrict
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                                                                                                                  content is in no way modified and this statement
Mus musculus.
                                              mRNA.
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(immunoglobulin-like)
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MGI; MGI:1321398; FIIr.
GO; GO:0005923; C:tight junction; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0007155; P:cell adhesion; IDA.
GO; GO:003085; P:epithelial cell differentiation; ID,
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig\_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG\_LIKE; 2. 3D-structure; Tight junction SIGNAL STRAND
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90 Glycoprotein; I n; Transmembrane 2.
; Immunoglobulin domain; Ig-like V-type 1.
Ig-like V-type 2.
N-linked (GlcNAc.
N-linked (GlcNAc... Potential.
Cytoplasmic (Potential). Junctional adl Extracellular Potential. adhesion (Potential). ここ Repeat; Signal; (Potential)

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RESULT 9
Q9JKD5 RAT
ID Q9JKD5;
AC Q9JKD5;
AC Q9JKD5;
DT 01-OCT-2000 (TrEMBLrel. 15, Care
DT 01-OCT-2003 (TrEMBLrel. 25, Las
DE Junctional adhesion molecule (I
GN Name=F11r;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; (
GN Namealia; Eutheria; Euarchontos
OC Mammalia; Eutheria; Euarchontos
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN NUCLEOTIDE SEQUENCE.
RN NUCLEOTIDE SEQUENCE.
RR Kirsch T., Wellner M., Haller H
Submitted (MAR-2000) to the EMEI
DR EMBL; AF241261; AAF61729.1; -;
DR SMR; Q9JKD5; 1-111.
DR RGD; 621842; F11r.
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 Kirsch T., Wellner M., Haller H., Lippoldt A.; submitted (MAR-2000) to the EMBL/GenBank/DDBJ EMBL; AF24126; AA61729.1; -; mRNA. HSSF; O86792; 1F97. HSSF; O86792; 1F97. SMR; Q9JKD5; 1-111. RGD; 621842; F11r.
                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                      EVSIHLTVLVPPSKPTISVPSSVTIGNRAVLTCSEHDGSPPSEYSWFKDGISMLTADAKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPT-NPKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGTEGKAGRKLLFLF-TSMILGSLVQGKGSVYTAQSDVQVPENESIKLTCTYSGFSSPRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EWKFVQGSTTALVCYNSQITAPYADRVTFSSSGITFSSVTRKDNGEYTCMVSEEGGQNYG
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68.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 1073.5; DB
; Pred. No. 5.5e-75;
44; Mismatches 49
                                                                                                                                                                                    Last sequence update)
Last annotation update
e (Fragment).
                                                                                                                                                                                                                             Created)
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                                                      databases
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                                                                                                                                   Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                             RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., A., Rubin G.M., Hong L.,
RA Hopkins R.F., Jordan H., Moore T., A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gunaratne P.H.,
RA Richards S., Worley N.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
"Generation and initial analysis of more than 15,000 full-length human rand mouse cDNA securences" "Generation and initial analysis of more than 15,000 full-length human
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Best Local
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InterPro; IPR003598; Ig_c2.
Pfam; PF00047; ig; 1.
SMART; SM00408; IGc2; 1.
PROSITE; PS50835; IG_LIKE; 1.
NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGC53721 protein.
Xenopus laevis (Airican clawed frog).
Xenopus laevis (Airican clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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TO XENLA
O7ZWTO_XENLA PRELIMINARY;
                                                                                                                                                  Richardson
                                                                                                                                                                           MEDLINE=22341132; PubMed=12454917; Klein S.L., Strausberg R.L., Wagner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                             TISSUE=Embryo;
                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
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                                                                                             initiative
                                                                                                                                                                                                                                                                                                                                                                mouse cDNA sequences.";
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                                                              225:384-391 (2002)
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                                                                                                                      for
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16; Mismatches
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Pred. No. 2.5e-46;
                                                                                                                                                                                  Wagner
                                                                                                                                                                                                                                                                                                                                    99:16899-16903 (2002).
                                                                                                                      Xenopus
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                                                                                                                                                                              DOI=10.1002/dvdy.10174; r L.. Pontius J., Clifton S.W.,
                                                                                                                         research:
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Q640CO_XENLA |

Q640CO;

Q640CO;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
LOC398627 protein (Fragment).

Name=LOC398627;
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphhba; Batrachia; Anura; Mesobatrachia; Pipoidea
MEDIINE-2338257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.;
                                                                                                                                                                                                                                                                                             Dev.
                                                                                                                                                                                                                                                                                                                                                                                               Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174; Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopodinae; Xenopus;
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SMART; SM00408; IGc2; 2.
PROSITE; PS50835; IG LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
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InterPro; IPR003598; Ig_c2.
                                                                                                                                                                                                                                             TISSUE=Kidney
                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
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SEQUENCE 289 AA; 31630 MW; 243541
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LOC398627 protein (Fragment).
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InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
INART; SM00409; IG; 2.
SMART; SM00408; IGc2; 2.
PROSITE; PSS0835; IG_LIKE; 2.
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          MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas. Strausberg R.L., Feingold E.A., Grouse L.H., Derge J Klausner R.D., Collins F.S., Wagner L., Shenmen C.M. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F
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Submitted (SEP-2004) to the EMI
EMBL; BC082710; AAH82710.1; -;
                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Ve
Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed
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Pred. No. 8.8e-37;
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Best Local :
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Q66172;
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711 receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klein S., Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BC05305; AR54305.1; -; mRNA.
HSSP; 088792; 1F97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
SMART; SM00408; IGc2; 1.
PROSITE; PS50835; IG_LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174; Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative.":
                                                                                                    13
BRARE
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                                                                                                                                                                        253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                     LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPS-ARSEGEFKQTSSFLV
                                                                                                                                                                                                                                        TIDPNTGVLKFASVGTSDSGEYYCKATNSQG-EQSSAIVRMDVKDVNVGGIVAAVVIVLL
                                                                                                                                                                                                                                                               VLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLI
                                                                                                                                                                                                                                                                                                         IVAPGTPVAQVPSSARTGSVABLMCVETQGPPLPTFTWYHNN--SPMQAKS----QNSTY
                                                                                                                                                                                                                                                                                                                                          LVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNSSY 188
                                                                                                                                                                                                                                                                                                                                                                                                          TRLVCYNNKITASYEDRVTFLFTGITFKSVTREDTGTYTCMVSEEGGN-SYGEVKVKLIV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILAILLC----SLALGSVTVHSSEPEVRIPENNPVKLSCAY-SGFSSPRVEWKF-DQGDT
                                                                                                                                                                                                                                                                                                                                                                          TSFVFYDGSLTASYKDRATSYPQGIKLNQVTRKDAGEYSCEVTSTGTKVLYGEAKIQLQV
                                                                                                                                                                                                                                                                                                                                                                                                                                             LLALLCCCCLWTAALAGVT--APDPTITVKEGDSPDLRCSYTSDYINPRVEWKFVNKDQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225:384-391 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 AA; 32858 MW; 02BC49DC74E271D4 CRC64;
                 (TrEMBLrel. 28, Created)
(TrEMBLrel. 28, Last seq
(TrEMBLrel. 28, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46; Mismatches
                   Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 580.5; DB Pred. No. 9e-37;
                                                                                    PRT;
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                 update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
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                                                                                                                                                                                                                                                                                                           193
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                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; 19; 1.
SMART; SM00409; IG; 2.
SMART; SM00408; IGc2; 2.
PROSITE; PS50835; IG LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZFIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0004872; F:receptor activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Director MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22388257;    PubMed=12477932;    DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Larvae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunoglobulin domain, Receptor.
SEQUENCE 292 AA; 32091 MW; E
                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.
                                                                            196
                                                                                                                206
                                                                                                                                                                                          146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BC081502; AAH81502.1; -; mF
ZDB-GENE-030131-2416; fllr.
                                                                                                                                                                                                                                  78
                                                                                                                                                                                                                                                                                                            21
                                                                                                                                                                                                                                                                                                                                                  29
                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
LPKLSETKQKPQAVYTQPQTDDVDEANGFRQKSSFVV
                                                                                                      DTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLILLGILVFGIWFAYSRGH
                                                                                                                                                      SSNVRLTCFDPVGSPPSTYKWYKDNTPLPEDPTKFPAFKNLTYKMNVFNGNLEFPSVSKM
                                                                                                                                                                                                                                                      RVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKVKLIVLVPPSKPTVNIPSSATI
                                                                                                                                                                                                                                                                                                          VIVIS---PVKVKENEGVDLQCSYTSDFGATPRVEWKFKDLKGSQTLVYFDGKPTGQYTG
                                                                                                                                                                                                                                                                                                                                    VTVHSSEPEVRIPENNPVKLSCAY-SGF-SSPRVEWKF-DQGDTTRLVCYNNKITASYED
                                      FDRTKKGTSSKKVIYSQPSARSEGE---FKQTSSFLV
                                                                          DTGSYFCEASNGEGVPQRGDEVKMEVRDLNVGGIVAGVIVALLAVGLLLFGLWYASKKGY
                                                                                                                                                                                          GNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNSSYVLNPTTGELVFDPLSAS
                                                                                                                                                                                                                                  RVTMYDKGLRFNKVTRADTGDYDCEVSGSGG---YGENTIKLTVLVPPAKPVSRIPSSVTT
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      37.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                      38;
                                                                                                                                                                                                                                                                                                                                                                                    Score 571.5; DB 2
Pred. No. 4.3e-36;
8; Mismatches 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E1F6B5FE74A72502 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                        105;
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                                                                                                                                                                                                                                                                                                                                                                                                                            292;
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M., Warrs R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M., Warrs R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M., Warrs M.A.,
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
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Best Local S
Matches 123
                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
Pfam; PF00047; Ig; 1.
SMART; SM00409; IG; 2.
SMART; SM00408; IGc2; 2.
PROSITE; PS50835; IG_LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (AUG-2004) to the EMBL/Gen EMBL; BC080901; AAH80901.1; -; mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Klein S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22388257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=MGC79514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGC79514 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin domain
SEQUENCE 291 AA; 3]
                                                                                                                                                                                                                                                                                 Local L
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 181
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                                                                                                                                                                                                                                                                                                                Similarity
                                                                                            GEVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEXTWFKDGIVMPTNPKS
                                    TRAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVI
                                                                       GEAKIQLLVIVAPSQPMAHVPNTVRTGSAVELRCVETQGYPPPTFTWYQNKAPMPPNPQ-
                                                                                                                                              FVNNQLETFFVYYDGTLTASYVNRATSVPQGIILNQITSKDAGEYSCEVTSVDSNGQTLY
                                                                                                                                                                               FDQGD-TTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNS----Y
                                                                                                                                                                                                                       ASSNRGAVVLGLLCACLWTAAFAGVS--TPNPTITVKQGATADLRCTYTSDFTKSRVEWK
                                                                                                                                                                                                                                                          AQVERKLICLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAY-SGFSSPRVEWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gerhard D.S.;
                                                                                                                                                                                                                                                                                             36.3%; Score 560.5; larity 40.9%; Pred. No. 3.1e Conservative 54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
-NATYTIDENTGVLKFRAVAASDSGDYYCKAANSEG-EQVSAIVRMNVQDVNVGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                        31538 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U.S.A.
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Last sequence update)
Last annotation updat
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RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Anthouard C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Crusud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Farra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
The early vertebrate proto-karyotype.";
Nature 431:946-957 (2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 110
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Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry whi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tetraodon nigroviridis (Green puffer).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 7 SCAF14703, whole genome shotgun sequen
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7. Carro1014703; CAG02884.1; -; Genomic_DNA.
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YSLDTELGKLTYSKTSLSDSGEYFCEAVNKAGPAQRCRAVKMEVRDLNTGGIVAGVIVAL
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tive 42; Mismatches 99
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RESULT 1  S56749  junctional adhesion molecule p N;Alternate names: F11 platele C;Species: Homo sapiens (man) C;Date: 27-Oct-1995 #sequence C;Accession: A59406; S56749 R;Ozaki, H; Ishii, K., Horiuc J. Immunol. 163, 553-557, 1999 A;Title: Cutting edge: combine A;Reference number: A59406; MU A;Accession: A59406 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-299 <oza></oza>		1500	1498	1497	1496	1495	1494	1493	1492	1491	1490
al adhes ate name ate homo ate type ate type ate homo ate home ate homo ate home ate homo ate		73.5	74	74	74	74	74	74	74	74	74
adhesion mol names: F11 iomo sapiens oct-1995 #se A59406; S5 ; Ishii, K.; ; Ishii, K.; tting edge: number: A59 a59406 number: A59 a59406 peliminary ype: DNA 1-299 < OZA>		44 ÷	4 4	4.	4.8	4.8	4.8	4.8	4.8	4.8	4.8
platel platel (man) 6749 Horiu 7, 199 combin		116	4476	3705	2508	1962	1483	1417	1417	1353	1251
precet a		<b>~</b> (	N K	N	N	N	N	N	N	N	N
RESULT 1  S16749  S16749  S16749  S16749  S10 Adhesion molecule precursor - human  S10 Adhesion molecule precursor - human  S10 Adhesion molecule pam-1;  C;Species: Homo sapiens (man)  C;Date: 27-Oct-1995 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004  C;Accession: A59406; S56749  R;Ozaki, H.; Ishii, K.; Horiuchi, H.; Arai, H.; Kawamoto, T.; Okawa, K.; Iw  J. Immunol. 163, 553-557, 1999  J. Immunol. 163, 553-557, 1999  A;Title: Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes  A;Reference number: A59406  A;Raccession:	ALIGNMENTS	HVMS1B	E71086	AD0123	S61441	A32634	C97012	D85521	H90670	T19691	T21389
RESULT 1  S156749  S156749  S156749  S156749  S156749  S156749  S1041 C; Species: And Eastlens (man)  C; Date: 27-Oct-1995 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004  C; C; Date: 27-Oct-1995 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004  C; C		Ig heavy chain pre	propable FFB proce	probable autotrans	surface-associated	lactocepin (EC 3.4	probably celluloso	probable adhesin e	probable invasin [		hypothetical prote

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F11

A;Cross-references: UNIPROT:Q9Y624; UNIPARC:UPI000000C1; GB:AAD42050; NID:g5326797; PI R;Naik, U.P.; Ehrlich, Y.H.; Kornecki, E. Biochem. J. 310, 155-162, 1995
A;Title: Mechanisms of platelet activation by a stimulatory antibody: cross-linking of a A;Reference number: S56749; MUID:95374438; PMID:7646439
A;Recession: S56749
A;Molecule type: protein
A;Residues: 28-49,'X',51-53;62-73,'E',75-103;123,'F',125-130;'FDKDXTIYLNXY';'LT',206,'X',A;Cross-references: UNIPARC:UPI00001468C7; UNIPARC:UPI00001468CD; UNIPARC:UPI00001468D1;
A;Note: the order of the peptides other than the amino terminus was not determined C;Genetics:
A;Note: the order of the peptides other than the amino terminus was not determined C;Genetics: JAM
C;Keywords: glycoprotein; phosphoprotein; platelet aggregation; platelet membrane F;1-25/Domain: signal sequence #status predicted <SIG>F;26-299/Product: junctional adhesion molecule #status predicted <MAT> 음 성 밁 ঠ 문 5 문 S 뭐 S Query Match Best Local Similarity Matches 299; Conserv 181 181 121 241 241 121 61 5 ᆫ AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSBGEFKQTSSFLV 299 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240 EVKVKLIVLVPPSKFTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180 EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYG EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYG EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 100.0%; Score 1544; DB 2; ilarity 100.0%; Pred. No. 3.3e-105; Conservative 0; Mismatches 0; Indels Length 299; 0 Gaps 120 120 60

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RESULT 3
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138346
clastic titin - human (fragment)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Coate: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C.Coate: 7. Coate: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C.Coate: 7. Coate: 7. Coate
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A;Title: Characterization of a cDNA encoding the bovine coxsackie and adenovirus
A;Reference number: JC7780
A;Contents: Liver
A;Accession: JC7780
A;Molecule type: mRNA
A;Residues: 1-365 <THO>
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A;Cross-references: UNIPROT:Q8WMV3; UNIPARC:UPI00000889CD; GB:AY033651
C;Comment: This protein serves as the primary adenoviral attachment site
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A;Cross-references: GDB:127867; OMIM:188840
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iophys. Res. Commun. 288, 805-808, 2001
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EDSGDYIC----EAHNGVGDASCSTALTVKAPPVFTQKPS---PVGALKGSDVILQC-EI
                                                             EDTGTYTCMVSEEGGNSYGEV--KVKLIVLVPP---SKPTVNIPSSATIGNRAVLTCSEQ 156
                                                                                                                           QGESIQLECKISGSPEIKVSWFRNDSELHESWKYN----MSFINSVALL----TINEASA
                                                                                                                                                                                     ENNPVKLSCAYSGESSPRVEWKEDQGDTTRLVCYNNKITASYEDRVTELPTGITEKSVTR 101
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J. Immunol. 151, 175-187, 1993
A; Title: Organization of the murine Cd22 locus. Mapping A; Reference number: I49583; MUID:93315834; PMID:8100843 A; Accession: I49583
A;Cross-references: UNIPARC:UPI000017C631
A;Experimental source: B cell lymphoma 38C13
A;Note: sequence extracted from NCBI backbone
                                                              A;Status: preliminary; not compared with A;Molecule type: nucleic acid A;Residues: 1-868 <TOR>
                                                                                                                                                   R;Torres, R.M.; Law, C.L.; Santos-Argumedo, L.; Kirkham, P.A.; Grabstein, K.; Parkhouse, J. Immunol. 149, 2641-2649, 1992
A;Title: Identification and characterization of the murine homologue of CD22, a B lympho A;Reference number: A46512; MUID:93017867; PMID:1401903
                                                                                                                                                                                                                                           RESULT 5
A46512
CD22 homolog/B lymphocyte-restricted adhesion molecule - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1995
C;Accession: A46512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P35329; UNIPARC:UPI0000027DD2; GB:L16928; NID:g348965; PIDN:1
C;Genetics:
A;Gene: CD22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-862 <RES>
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149583
differentiation antigen - mouse
differentiation antigen - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGT----PMTSNAVRMEAVERNVGVI 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IVLVPPSKPTVNIPSSATI--GNRAVLTCSEQDGSPP-SEYTWFKDGIVMPTNPKSTRAF 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----KNGSLV--QEGRY-----LSFGSVSPEDSGNYNCMVN----NSIGETLSQAWNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VAAVLVTLILLGILVFGIW 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSSGQDLHSSGQKLRLEPLEVQHTGSYRCKGTNGIGTGESPPST----LTVYYSPETIGKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVLYAPRRLRVSISPGDHVMEGKKATLSC-ESDANPPISQYTW------P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKVK---L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CSLALGSV-TVHSSEPEVRIPENNP-----VKLSC--AYSGFSSPRVEWKFDQGDT
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                                                                                                                                                                                                                                                                                                                                                                                                                               VALGEG--FCLTICILAIW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATNEVGSDTCSCSVKFKEPPRFVKKLSDTSTLIGDAVELRAIVEGFQPISVVWLKDRGEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               719
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                                                                                                            conceptual
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                                                                                                                 translation
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(NCBIP: 116156)

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vascular cell adhesion protein - pig
(;Species: Sus scrofa domestica (domestic pig)
C;Date: 15-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C;Accession: JC2457
R;Tsang, Y.T.M.; Haskard, D.O.; Robinson, M.K.
Biochem. Biophys. Res. Commun. 201, 805-812, 1994
A;Title: Cloning and expression kinetics of porcine vascular cell adhesion n
A;Reference number: JC2457; MUID:94271236; PMID:7516159
A;Accession: JC2457; MUID:94271236; PMID:7516159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Keywords: glycoprotein; transmembrane protein F;497-517/Domain: transmembrane #status predicted <TVM>F;75,157,271,330,360/Binding site: carbohydrate (Asn) (
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A; Residues: 1-538 < TSA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSWALPVILNVHYAPROVKVLKVSPASEIRAGQRVLLQCDFAESNPAEVRFFWK-----
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                                             SSLIIPAIGVIIYFARKANMRGSY 528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVLYAPRRLRVSIIPGDHVMEGKKATLSC-ESDANPPISQYTW------F
                                                                                    --TLIL--LGILVFGIWFAYSRGHF 266
                                                                                                                                                                    VLNPTTGBLVFDPLSASDTGBYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLV---
                                                                                                                                                                                                                                                                                                                                                                                  ---ATLTLIAMRMEDSGIYVC----EGVNPVGTNRKEVELTVQVAPRDTTISVNPSSTLE
                                                                                                                                                                                                                                                                                                                                                                                                                         FLPTGITFKSVTREDTGTYTCMVSEEGGNSYG--EVKVKLIVLVPPSKPTVNIPSSATI- 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VAAVLVILILLGILVFGIW 258
                                                                                                                           VLKSTDGAYTIHRARLADAGVYECESKNEIGLQLRSITLDVKGRESNKDYFSSELLVLYC
                                                                                                                                                                                                               AGINRKEVELIIQAAPKDLQLTAPPSESVKEGDTVIISCTCGNVPPTLIILKKKAETGDT
                                                                                                                                                                                                                                                        -----RAFSNSSY-----
                                                                                                                                                                                                                                                                                               EGSSVNMTCS-SDGFPAPKILWSKKLRDGNLEPLSENTTLTLTSTKMEDSGIYVCEGINQ
                                                                                                                                                                                                                                                                                                                                         -GNRAVLTCSEQDGSPPSEYTWFK---DGIVMPTNPKST-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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21.5%;
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hypothetical protein DKFZp586O1624.1 - human (fragment) C;Species: Homo sapiens (man) C;Date: 15-Oct-1999 #text_chang C;Date: 15-Oct-1999 #text_chang C;Accession: T17346 C;Accession: T17346 R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; submitted to the Protein Sequence Database, September 1999
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A;Cross-references: GDB:127545; OMIM:107266
A;Map position: 19613.1-19613.1
A;Introns: 138/1; 240/1; 329/1; 417/1; 503/1; 591/1; 679/1; 711/2; 804/3
A;Introns: 138/1; 240/1; 329/1; 417/1; 503/1; 591/1; 679/1; 711/2; 804/3
C;Keywords: alternative splicing; B-cell; cell adhesion; dimer; glycoprotein; phos F;1-19/Domain: signal sequence #status predicted <SIG-F;1-19/Domain: signal sequence #status predicted signal sequence #status predicted signal sequence #status predicted signal sequence #status predicted signal sig
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A;Title: Genomic structure and chromosomal mapping of the human CD22 gene. A;Reference number: 156171; MUID:93267103; PMID:8496602
A;Accession: I56171
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B-cell adhesion protein CD22 beta splice form precursor - human
N;Alternate names: B-cell membrane protein CD22
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: JH0371; 156171

R;Wilson, G.L.; Fox, C.H.; Fauci, A.S.; Kehrl, J.H.

J. Exp. Med. 173, 137-146, 1991

A;Title: CDIA cloning of the B cell membrane protein CD22: a mediator of A;Reference number: JH0371; MUID:91086838; PMID:1985119

A;Accession: JH0371
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A;Residues: 121-269,'T',271-473,'K',475-614,'R',616-638,'Y',640-711,777-847 <WIL2>
A;Cross-references: UNIPARC:UPI00006EB4A; GB:S61375; NID:g385980; PIDN:AAC18956.1;
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A; Residues: 1-847 <WILl>
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          551 GKESQLNFDSISPEDAGSYSCWVN----NSIGQTASKAWTLEVLYAPRRLRVSMSPGDQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEGKSATLTC-ESDANPPVSHYTWFD------WNNQS--LPHHSQKLRLEPV
                                                                                                             WFAYSRGHFDRTKKGTSSKKVIYSQPSARS 287
                                                                                                                                                                                                                          KVQHSGAYWCQGTNSVGKGRSPLSTLTVYYSPETIGRRVAVGLGSCLAILIL---AICGL
                                                                                                                                                                                                                                                                                                                                        SASDTGEYSCEARNGYG---TPMTSNAV--RMEAVERNVGVIVAAVLVTLILLGILVFGI 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --GNRAVLTCSEQDGSPP-SEYTWFKDGIVMPTNPKSTRAFSNSSYVLNPTTGELVFDPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKVK---LIVLVPPSKPTVNIPSSATI 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VRVRKIKPLSEIHSGNSVSLQCDFSSSHPKEVQFFWEK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VTVHSSEPEVRIPENNPVKLSCAYSGFSSPRVEWKFDQGDTTRLVCYNNKITASYEDRVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
-KLORRWKRTOSOOGLOENSSGOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.6%; Score 178.5; DB 2; 25.6%; Pred. No. 2.7e-05; tive 42; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59;
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15-Oct-1999 #text\_change 09-Jul-2004

Wiemann,

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A;CCOSS-Teferences: UNIPARC:UPI0000159270; GB:X52785; NID:g29778; C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
GDB:CD2
A;Cross-references: GDB:127545; OMIM:107266
A;Map position: 19q13.1-19q13.1
C;Keywords: alternative splicing; B-cell; cell adhesion; dimer; glC;Keywords: alternative splicing; B-cell; cell adhesion; dimer; glF;1-19/Domain: signal sequence #status predicted <SIG>F;20-510/Domain: extracellular #status predicted <EXIV>F;30-549/Domain: transmembrane #status predicted <CYT>F;51-29/Domain: intracellular #status predicted <CYT>F;530-647/Domain: intracellular #status predicted <CYT>F;67,101,112,135,164,231,268,302,397,457/Binding site: carbohydrat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: Z18727
A;Accession: T17346
A;Status; preliminary
A;Molecule type: mRNA
A;Residues: 1-483 <DUE>
A;Cross-references: UNIPROT:09UFI4; UNIPARC:UPI00000726A2; EMBL:AL117666
A;Experimental source: adult uterus; clone DKFZp58601624
C;GenetLcs:
A;Note: DKFZp58601624.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: The B-cell antigen CD22 mediates | A;Reference number: A35648; MUID:90231465; A;Accession: A35648 A;Molecule type: mRNA A;Residues: 1-647 <STA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B-cell adhesion protein CD22 alpha splice form precursor - C;Species: Homo sapiens (man) C;Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_ch C;Accession: A35648 R;Stamenkovic, I:; Seed, B. Nature 345, 74-77, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
A35648
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                                                                                                                                                                                                 Query Match
Best Local S
Matches 69
                                                                                                                                                                                                                                                                                           ;511-529/Domain: transmembrane #status predicted <TWM>;530-647/Domain: intracellular #status predicted <CYT>;67,101,112,135,164,231,268,302,397,457/Binding site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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374 GKESQLNFDSISPEDAGSYSCWVN----NSIGQTASKAWTLEVLYAPRRLRVSMSPGDQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             265 HFDRT------KKGTSSKKVIYSQPSARSEG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 RAHSQLSVLPAAGCRKDGTTVGIFTIAVVSSIVLTSL----VWVCIIYQTRKKSEEYSVT 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47 KLSCAYSGFSSPRVEWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITF--KSVTREDT 104
                                                                                                                                                                                                   69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68;
                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                FLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKVK---LIVLVPPSKPTVNIPSSATI 145
                                                                                                                                                  VTVHSSEPEVRIPENNPVKLSCAYSGFSSPRVEWKFDQGDTTRLVCYNNKITASYEDRVT 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NTDETVVPPDVPSYLSSQGTLSDR---QETVVRTEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MTSN-----AVRMEAVERNVGVIVAAVLVTLILLGILVFGIWFA-------YSRG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RITWF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EYTWFKDGIVMPTNPKSTRAFS-NSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTP 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVYSCTAQ----NSAGSISANATLTVLETPSLVVPLEDRVVSVGETVALQC-KATGNPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTYTCMVSEEGGNSYGEVKVK--LIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLECAATGHPNPQIAWQKDGG-----TDFPAARERRMHVMPDDDVFFITDVKIDDA
                                                                                                 VRVRKIKPLSEIHSGNSVSLQCDFSSSHPKEVQFFWEK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.5%; Score 178; DB 2; I
ilarity 24.6%; Pred. No. 1.6e-05;
Conservative 32; Mismatches 112;
                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----KGDRPLSLTERHHLTPDNQLLVVQNVVAEDAGRYTCEMSNTLGTE 162
                                                                                                                                                                                                                     11.5%;
25.6%;
                                                                                                                                                                                                   42;
                                                                                                                                                                                              Score 177.5; DB 2; Pred. No. 2.4e-05; 2; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            monocyte and PMID:1691828
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                                                                                                                                                                                                                                                                                                   (Agn)
                                                                                                                                                                                                                                                                                                   (covalent)
                                                                                                 373
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R;Zallen, J.A.; Y1, B.A., Zuner, Edi 92, 217-227, 1998 Cell 92, 217-227, 1998 Cell 92, 217-27, 1998 Immunoglobulin superfamily member SAX-3/Robo A;Title: The conserved immunoglobulin superfamily member SAX-3/Robo PMID:9458046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sax-3 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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A; Residues: 1-1273 <Z/
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                                                                                                                                                                                                                                                                                           64 YKDGQPVITNKEQVNSHRIV------LDTGSLFLLKVNSGKNGKDSDAGA 107
                                                                                                                                                                                                                                                                                                                           63 KFD-----QGDTTRLVCYNNKITASYEDRVTFLPTGITF------KSVTREDTGT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                      ; 88
                                                                                                                                                                                                                                                                                                                                                                 ហ
                                                                                                                                                                                                                                                                                                                                                                                                   9 RKLLCLFILAI-----LLCSLALGSVTVHSSEP-EVRIPENNPVKLSCAYSGFSSPRVEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                   YYCVAS----QALGGEWAVLECSPP 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --GNRAVLTCSEQDGSPP-SEYTWFKDGIVMPTNPKSTRAFSNSSYVLNPTTGELVFDPL
 EPMPVTRAYIAKDNRGLRIERV---QPS--DEGEY
                                                                     MVG-ERVSNPARLSVFEKPKFEQEPKDMTVDVGAA----VLFDCRVTGDPQPQITWKRKN
                                                                                                         GYGTPMTSNAVRMEAVE-----RNVGVIVAAVLVTLILLGILVFG-----IW----
                                                                                                                                                                               DGSPPSEYTWFKDGIVMPTNPKSTRAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARN
                                                                                                                                                                                                                                                       YTCMVSEEGGNSYGEVK-----VKLIVL-----VPPSKPTVNIPSSATIGNRAVLTCSEQ 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEGKSATLTC-ESDANPPVSHYTWFD--
                                   -- FAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEF
                                                                                                                                             RGFPEPVVSWRKD------DKELRIQDMPRYTLH-SDGNLIIDPVDRSDSGTYQCVANN
                                                                                                                                                                                                                                                                                                                                                                 KTLLCTILLVLQAVIRSFCEDASNLAPVIIEHPIDVVVSRGSPATLNCGAKP-STAKITW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SASDTGEYSCEARNGYG---TPMTSNAV--RMEAVERNVGVIVAAVLVTLILLGILVFGI 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sax-3 function is required at the time of
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 177.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           No.
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                                     291
 294
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                                                                       264
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                                                                                                             258
                                                                                                                                                 209
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R;Kershaw, J.
submitted to the EMBL Data Library, November A:Reference number: Z19651

A;Accession: T23004 A;Status: preliminary; translated

from GB/EMBL/DDBJ

hypothetical protein F59F3.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004 C;Accession: T23004

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F;36-61/Domain: proteoglycan amino-terminal homology <PAH;
F;71-94/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;95-117/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;18-141/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;118-141/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;142-165/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;166-189/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;214-237/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;214-237/Jomain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;214-237/Jomain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;262-285/Jomain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;263-399/Jomain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F;310-333/Jomain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F;385-408/Jomain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F;385-408/Jomain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F;398-408/Jomain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F;409-432/Jomain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
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A58532
A58532
C;Species: Mus musculus (house mouse)
C;Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change
C;Accession: A58532
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A;Cross-references: UNIPROT:P70193; UNIPARC:UPI0000029E57; GB:D78572; NID:g1545806; PIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Suzuki, Y.; Sato, N.; Tohyama, M.; Wanaka, A.; Takagi, T.
J. Biol. Chem. 271, 2522-2527, 1996
A;Title: CDNA cloning of a novel membrane glycoprotein that is
A;Reference number: A58532; MUID:96394313; PMID:8798419
A;Accession: A58532
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A;Residues: 1-1227 <MIL>
A;Residues: 1-1227 <MIS
A;Cross-references: UNIPROT:Q21038; UNIPARC:UPI0000077D8B; EMBL:Z68005; PIDN:CAA91990.1
A;Experimental source: clone F59F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
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EVRIPENNPVKLSCAYSGESSPRVEWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITF:: | : | : | : | : | | : : |
                                                                                                                                                                                                                                                                                                    in: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
in: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
in: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
in: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
in: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
in: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
in: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
in: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
in: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
in: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
in: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
in: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
in: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
in: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
in: leucine-rich alpha-2-glycoprotein repeat homology <LR14-1>
in: leucine-rich alpha-2-glycoprotein repeat homology <LR14-1>
in: leucine-rich alpha-2-glyc
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                                                                                                                                                                  11.1%; Score 171; 23.5%; Pred. No. 0
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                                                                                                                             Pred. No. 0.00
3; Mismatches
                                                                                                                                                                  DB 2;
0.00013;
                                                                                                                                                                                                   Length 1091;
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                                                                                                             cell adhesion molecule apCAM (clone d15) - California sea hare (Species: Aplysia californica (California sea hare) C;Species: Aplysia californica (California sea hare) C;Accession: B42632 R;Mayford, M.; Barzilai, A.; Keller, F.; Schacher, S.; Kandel, E.R. Science 256, 638-644, 1992 R;Mayford nof an NCAM-related adhesion molecule with long-term synup, Reference number: A42632; MUID:92263095; PMID:1585176
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                                            A; Status: preliminary; not con A; Molecule type: nucleic acid
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RESULT 13
C42632
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C;Species: Aplysia californica (California sea hare)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_chang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid A;Residues: 1-765 <MAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Note: sequence extracted from NCBI backbone (NCBIP:101351)
C; Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q9TWA4; UNIPARC:UPI000007CFAFA;Experimental source: CNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 256, 638-644, 1992
A;Title: Modulation of an NCAM-related adhesion molecule
A;Reference number: A42632; MUID:92263095; PMID:1585176
A;Accession: C42632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Mayford, M.; Barzilai, A.; Keller, F.; Schacher, S.; Kandel, E.R.
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                                                                                                    TIKGG--FAESSNTLDVKVPPTIEDMEETYDAVSGQELTITCTAK-GDPEPSVIWKKDGP
QSASTDGIVNKGPTYEKVGSNQNDMEEKTVAQHMTFKPVTYQDAGTYICTA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIAIRTGTTARLECAATGHPNPQIAWQKDGG-----TDFPAARERRMHVMPDDDVF
                                                                                                                                                                                                                                                               FSSPRVEWKFDQGD---TTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMV 111
                                                                                                                                                                                                                                                                                                                        KKYLCDIIVIDTGETKDFYIDFTVVKLPTIAL-PPTIHPDNPKV-----GDEVKITCQATG
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                                                   -----VMPTNPKSTRAFSNSSYVLNPTTGE-LVFDPLSASDTGEYSCEA 214
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RESULT 15
A42632
Coell adhesion molecule apCAM (clone d19) - California sea hare
Coell adhesion molecule apCAM (clone d19) - California sea hare
Coell adhesion molecule apCAM (clone d19) - California sea hare
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A;Experimental source: CNS
A;Note: sequence extracted from NCBI backbone (NCBIP:101342)
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
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A;Experimental source: CNS
A;Note: sequence extracted from NCBI backbone (NCBIP:101346)
A;Note: sequence extracted from NCBI backbone (NCBIP:101346)
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
Search completed: May 16, 2006, 07:03:28 Job time : 64 secs
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Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY23321 standard; protein; 299 AA.
Amino acid sequence of the PRO301 polypeptide.
 AAY70670 standard; protein; Human PRO301 protein.
                                                                                                                                                                                                                                                                                                                                                                                             F11 antigen protein sequence. WO9902561-A1.
                                                                                        WO9955865-A1.
                                                                                                 AAY76076 standard; protein; 299 AA.
Human A33 receptor homologue, SEQ ID
                                                                                                                                                                (GENE-) GENESIS RES
                                                                                                                                                                            04-NOV-1999:
                                                                                                                                                                                       Human A33 receptor WO9955865-A1.
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May 16, 2006, 07:03:43; Search time 187 Seconds
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                                                                                   Human immune response WO200119991-A1. 22-MAR-2001.
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AAU12354 standard; protein; 299 AA. Human PRO301 polypeptide sequence. WO200140466-A2.
                                                                                                                                                                                     AAB31202 standard; protein; 299 AA. Amino acid sequence of human polype WO200077037-A2.
21-DEC-2000.
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Skin cell protein,
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EP1130094-A2.
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Human PRO301 protein.
WO200104311-A1.
18-JAN-2007.
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Human PRO301 protein sequence SEQ
WO200032221-A2.
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Skin cell protein, SEQ ID NO: 189.
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ry Match 100.0%; Score
t Local Similarity 100.0%; Pred.
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Human polypeptide, SEQ ID NO: 3365.
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Human gene 23 encoded secret
WO200136440-A1.
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w0200053753-A2.
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WO200155437-A2.
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Human novel protein #276.
Human PRO301 protein WO200200690-A2.
                                                                    Human polypeptide WO200190304-A2.
                                                                                     ABB90290 standard;
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Human novel protein #39.
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                  ABB84843 standard;
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ry Match 100.0%;
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(HYSE-) HYSEQ INC.
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US2003032156-A1.
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Human PRO polypeptide #21.
US2002146709-A1.
10-OCT-2002.
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                  ABO47382 standard; protein; 2 Human secreted/transmembrane US2003044839-A1.
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US2002177165-A1.
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Human A-33 related antigen PRO301.
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Human junctional adhesion molecule
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ADB19374 standard; protein; 299 AA
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Human PRO polypeptide #183.
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Human PRO polypeptide #183.
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(GETH ) GENENTECH INC.
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Human PRO polypeptide #183.
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US2003082761-A1.
01-MAY-2007
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                                                                                        ADA46989 standard; protein;
Human PRO polypeptide #183.
US2003073210-A1.
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Human PRO polypeptide #183.
US2003073214-A1.
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Human PRO polypeptide #21.
US2003064367-A1.
ADB25285 standard, protein; 2
Human PRO polypeptide SEQ ID
US200307715-A1.
24-APR-2003.
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Novel human secreted and transmembrane protein PRO301
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01-MAY-2003.
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Human PRO polypeptide #183.
US2003092147-A1.
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Human PRO polypeptide #183.
US2003082702-A1.
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Human PRO polypeptide #183.
US2003082690-A1.
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Human PRO polypeptide SEQ ID
US2003077714-A1.
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US2003049817-A1.
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Human PRO polypeptide #183.
US2003096386-A1.
22-MAY-2003.
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24-APR-2003.
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                                 ADB26259 standard; protein;
Human PRO polypeptide #183.
US2003082760-A1.
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                                                                                                  ADA88049 standard; protein; 299 AA. Novel human secreted and transmembrane US2003082700-A1.
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13-MAR-2003.
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Human secreted/transmembrane
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US2003082686-A1.
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US2003059909-A1.
27-MAR-2003
                                                               ADB22296 standard; protein; 299 AA.
Novel human secreted and transmembrane
US2003087344-A1.
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Human PRO polypeptide #183.
US2003022239-A1.
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Human PRO polypeptide #183.
US2003082706-A1.
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Human PRO polypeptide #183.
US2003082699-A1.
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  Human
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Novel human secreted and transmembrane protein PRO301
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ABO19860 standard; protein; 299 AA.
Human secreted/transmembrane protein
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Best Local Similarity
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PD 03-APR-2003.
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US2003082712-A1.
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US2003082766-Al
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US2003077711-A1.
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Human PRO polypeptide #21.
US2003064923-A1.
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Human PRO polypeptide #183.
US2003068793-A1.
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06-MAR-2003.
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Novel human secreted and transmembrane
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US2003082698-A1.
01-MAY-2003.
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Human PRO polypeptide #183.
US2003082762-A1.
ADB34483 standard; protein; 299
Human PRO polypeptide SEQ ID NO
US2003077717-A1.
24-APR-2003.
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01-MAY-2003.
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Human PRO polypeptide #183.
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US2003082687-A1.
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Pred. No. 7.5e-105;
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Query Match
Best Local Similarity
RESULT 150
ID ADC18969 standard; p
DE Human secreted/trans
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH IN
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Human secreted/transmembrane
US2003059772-A1.
27-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADB36139 standard; protein;
Human PRO polypeptide SEQ II
US2003077720-A1.
                     Human secreted/transmembrane US2003036061-A1.
                                                                                                           ADC40141 standard; protein; 2
Human secreted/transmembrane
US2003059829-A1.
                                                                                                                                                                                                   Human secreted/transmembrane US2003059828-A1.
                                                                                                                                                                                                                         ADC39627 standard; protein; 299 AA
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Human PRO polypeptide SEQ ID NO 366.
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Human PRO polypeptide SEQ ID
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GENENTECH INC

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Best Local Similarity RESULT 158
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RESULT 152
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13-MAR-2003.
(GETH ) GENENTECH INC.
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                                                                                                                                          ADC50407 standard; protein; 299 AA.
Novel human secreted and transmembrane
US2003092106-A1.
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Human secreted/transmembrane
US2003073079-A1.
17-APR-2003.
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Human secreted/transmembrane
US2003036094-A1.
20-FEB-2003.
                                      ADC71954 standard; protein; 299 AA. Novel human secreted and transmembr US2003092107-A1.
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Human secreted/transmembrane
US2003049676-A1.
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Human secreted/transmembrane protein,
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RESULT 165
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US2003087359-A1.
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US2003087363-A1.
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US2003087365-A1.
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Human PRO polypeptide #183.
US2003087362-A1.
08-MAY-2003.
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                                                                                                 ADC53546 standard; protein; 299 AA. Novel human secreted and transmembrane
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                                                                                US2003087364-A1.
08-MAY-2003.
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RESULT 172
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ID ADC55947 standard;
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Human PRO polypeptide #183.
US2003194770-A1.
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                               US2003087354-A1.
08-MAY-2003.
                                                   ADD04595 standard; protein; 299 AA. Novel human secreted and transmembrane
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Human PRO polypeptide #183.
US2003194773-A1.
16-OCT-2003.
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Human secreted/transmembrane
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US2003087358-A1.
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Human secreted/transmembrane
US2003105011-A1.
 ADD03500 standard;
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Human secreted/transmembrane protein,
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Human secreted/transmembrane
US2003105013-A1.
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Human PRO polypeptide #183.
US2003194774-A1.
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(GETH ) GENENTECH INC.
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30-CCT-2003.
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Human PRO polypeptide #183.
US2003194792-A1.
16-OCT-2003.
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Human PRO polypeptide #183.
US2003194769-A1.
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ADD54183 standard; protein; 299 AA.
Novel human secreted and transmembr
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US2003203432-A1.

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RESULT 204
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RESULT 197
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RESULT 199
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US2003203428-A1.
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US2003199056-A1.
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Human PRO polypeptide #183.
US2003199057-A1.
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Human PRO polypeptide #183.
ADD91948 standard; protein; 299
Human PRO polypeptide #183.
US2003199053-A1.
                                                                                      ADE17816 standard; protein;
Human PRO polypeptide #183.
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Human PRO polypeptide #183.
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US2003199033-A1.
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US2003199026-A1.
23-OCT-2003
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ADD95905 standard; protein;
Human PRO polypeptide #183.
US2003199059-A1.
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Human secreted/transmembrane
US2003077583-A1.
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US2003199025-A1.
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Human PRO polypeptide #183.
US2003207417-A1.
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16-OCT-2003.
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Novel human secreted and transme
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US2003199031-A1.
23-OCT-2007
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           Human PRO polypeptide #183.
US2003194777-A1.
                                                                                         ADE04678 standard; protein;
Human PRO polypeptide #183.
US2003199034-Al.
23-OCT-2003.
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Human PRO polypeptide #183.
US2003199032-A1.
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Human PRO polypeptide #183.
US2003199028-A1.
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Human PRO polypeptide #183.
US2003207418-A1.
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Novel human secreted and transmembrane protein PRO301
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                                         ADH59235 standard; protein; 299 AA. Human secreted/transmembrane protein, US2003039972-A1.
27-FEB-2003.
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Human PRO polypeptide #183.
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Human PRO polypeptide #183.
US2003207370-A1.
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Human PRO301 protein.
US2003171568-A1.
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Human secreted/transmembrane polypeptide
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RESULT 233
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ID ADI38014 standard, p
DE Human secreted/trans
PN US2003054352-A1.
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ID ADI640
DE Novel
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Novel human secreted and transmembrane
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                                                                     ADD87915 standard; protein;
Human PRO polypeptide #183.
US2003092113-A1.
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Human PRO polypeptide #183.
US2003100087-A1.
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Human secreted/transmembrane protein,
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17-JUL-2003.
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US2003092115-A1.
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US2003092108-A1.
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                ADE89229 standard;
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US2003211571-A1.
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RESULT 262
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                                                                              Human PRO polypeptide #183. US2003199052-A1. 23-OCT-2003.
Human PRO polypeptide #183. US2003199060-A1.
                                                                                                                                                                          ADE91108 standard; protein;
Human PRO polypeptide #183.
US2003199061-A1.
23-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADE18368 standard; protein;
Human PRO polypeptide #183.
US2003194794-A1.
                                                                                                                                                                                                                                                                 ADE94697 standard; protein;
Human PRO polypeptide #183.
US2003199027-A1.
23-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                     Human secreted/transmembrane US2003211576-A1.
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Human PRO polypeptide #183.
US2003199054-Al.
23-OCT-2003.
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05-JUN-2003.
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Human secreted/transmembrane polypeptide
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(GODD/) GODDARD A.
(GODD/) GODWSKI P J.
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(MATH/) MATHER J P.
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US2003199029-A1.
                                                         Human secreted/transmembrane US2003180312-A1.
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Human secreted/transmembrane
US200325253-A1.
04-DEC-2003.
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Novel human secreted and transmembrane
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Human PRO polypeptide #183.
US2003199063-A1.
23-OCT-2003.
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Novel human secreted and transmembrane protein PRO301
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Human secreted/transmembrane protein,
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                             Human PRO polypeptide #183.
US200320739-A11.
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                                                                                                               ADF99167 standard; protein;
Human PRO polypeptide #183.
US2003207353-A1.
                                                                                                                                                                                          ADG03446 standard; protein;
Human PRO polypeptide #183.
US2003207351-A1.
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Human PRO polypeptide #183.
US2003208055-A1.
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                                                                                                                                                                                                                                                                                                                                                           ADG24261 standard; protein; 299 AA. Novel human secreted and transmembrane
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Human PRO polypeptide #183.
US2003207376-A1.
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US2003207371-A1.
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US200321985-A1.
27-NOV-7009
ADG03998 standard; protein;
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Human secreted/transmembrane
US2003027145-A1.
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Novel human secreted and transmembrane
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Human PRO polypeptide #183.
US2003194793-A1.
16-OCT-2003.
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Novel human secreted and transmembrane
US2003207416-A1.
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Human secreted/transmembrane polypeptide PRO301.
US2003180796-A1.
                  ADG61459 standard; protein; 299 AA. Novel human secreted and transmembrane US2003207429-A1.
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Novel human secreted and transmembrane
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US2003224984-A1.
04-DBC-2003.
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Human secreted/transmembrane protein,
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Human secreted/transmembrane protein,
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Novel human secreted and transmembrane
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Novel human secreted and transmembrane
US2004009548-A1.
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Human PRO polypeptide #183.
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(GODD/) GODDARD A.

(GODO/) GODOWSKI P J.

(GURN/) GURNEY A L.

(MATH) MATHER J P.

(WILL/) WILLIAMS P M.

(WOOD/) WOOD W I.
                                                                                                  ADM25082 standard; protein; i
Human secreted/transmembrane
US2003096233-A1.
                          Human platelet
US6699688-B1.
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                                   ADK40844 standard;
Human platelet F11
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Human secreted/transmembrane protein,
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US200403335-A1.
26-FER-2000
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          Human PRO polypeptide #183. US2004048333-A1.
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RY Match 100.0%; Sc
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Human PRO polypeptide #27.
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Albumin fusion protein related therapeutic
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Albumin fusion protein related therapeutic protein
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US2004077064-A1.
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US2004058424-Al.
25-MAR-2004
                             Human secreted/transmembrane US2004147017-A1.
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(ASAH-) ASAHI KASEI PHARMA CORP.
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WO2004031105-A2.
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              02-SEP-2004
(DOKU-) DOKI
                                                                            (DOKU-) DOKURITSU GYOSBI HOJIN KAGAKU GIJUTSU ry Match 100.0%; Score 1544; DB t. Local Similarity 100.0%; Pred. No. 7.5e-1
                                                                                                            02-SEP-2004
                                                                                                                        ADR46571 standard; protein; 299 AA.
Human JAM-1, F11 receptor (F11R) transcript variant
JP2004242513-A.
                                                                                                                                                                    (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH. ry Match 100.0%; Score 1544; DB 8; t Local Similarity 100.0%; Pred. No. 7.5e-105;
                                                                                                                                                                                                                            ADR46577 standard; protein; 299 AA.
Human JAM-1, F11 receptor (F11R) transcript
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Human PRO polypeptide #183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADR27641 standard; protein; 299 Human F11 receptor protein Seq WO2004063327-A2.
                                            ADR46573 standard; protein; 299 AA.
Human JAM-1, Fll receptor (FllR) transcript
                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC.
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BABI/) BABINSKA
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GODOWSKI P J.
GRIMALDI C J.
GURNEY A L.
HILLAN K J.
KLJAVIN I J.
            DOKURITSU
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EATON D L.
FERRARA N.
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STEWART T A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GERBER H.
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Score 1544; DB 8;
Pred. No. 7.5e-105;
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ADU06480 standard; protein; 299 AA.

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02-SEP-2004.
(DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU:
100.0%; Score 1544; DB
100.0%; Pred. No. 7.5e-1
                         ADT03591 standard; protein; 2
Human secreted/transmembrane
US200315922-A1.
14-AUG-2003.
                                                                                                  Human PRO polypeptide #183.
US2004214269-A1.
28-DCT-200
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Human JAM-1, F11 receptor (F11R) transcript variant
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AU2003259607-A1.
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JP2004242513-A.
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Novel human secreted and transmembrane
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                  GETH )
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FERRARA N.
FILVAROFF E.
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BOTSTEIN D.
DESNOYERS L.
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GRIMALDI C J.
GURNEY A L.
HILLAN K J.
                                                                                      GENENTECH INC.
Similarity
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Human secreted/transmembrane protei
US2005112725-A1.
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03-PEB-2005.
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Novel bronchial car
DE10316701-A1.
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(HERM/) HERMANN K.
(CAST/) HEIDEN CASTANOS-VELEZ
                                                                                                                                           (NAST-) NASTECH PHARM CO INC.
ry Match 100.0%;
t Local Similarity 100.0%;
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                                           (DEFO/)
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                                                                                                 US2005153396-A1.
                                                                                                                      AEB14083 standard; protein;
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(HERM/) HERMANN K.
(CAST/) HEIDEN CASTANOS-VELEZ E.
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GERRITSEN M E.
GODDARD A.
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cancer-associated human
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(WANG/) WANG Z.
(WENG/) WENG G.
(BOYL/) BOYLE B J.
(DRMA/) DRMANAC R T.
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(WANG) WANG Z.

(WENG) WENG G.

(BOYL) BOYLE B J.

(DRMA) DRMANAC R T.
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                                                                                                                                                                                                                                                      Novel human polypeptide seq
US2004219521-A1.
                ADH80723 standard; protein;
Human polypeptide #40.
US2003232054-A1.
                                                                            ADC78439 standard; protein;
Human PRO301 protein.
WO200015796-A2.
23-MAR-2000.
                                                                                                                                                       AAY08071 standard; protein;
Human PRO307 protein.
WO9914241-A2.
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(HYSE-) HYSEQ INC.
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STEWART T A.
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                                                   1539;
No. 1.
                                                                                                                      1540;
No. 1.
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No. 8.
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No. 8.
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No. 8.
                                                                                                                                                                                          1544;
No. 8.
                                                                                                                                                                                                                                                                                                                                        genetic
                                                   1.7e-104;
                                                                                                                       1.5e-104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 7;
3.1e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence
                                                                                                                                                                                                                                                                                                                                                                 DB 9;
1.1e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9;
                                                                                                                                                                                          DB 9;
.6e-105;
                                                                                                                                                                                                                                                                                                DB 7;
.6e-105;
                                                                                                                               BB
                                                                                                                                                                                                                                                                                                                                         disorders)
                                                           Length
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                                                                                                                                                                                                 Length 336;
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                                                            299;
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TANG Y T.

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Query Match
Best Local S
RESULT 397
                                                                              RESULT 398
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RESULT 396
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                                                                                                                                                                                                                                                                                                      RESULT 395
      Query Match
                                                                                        Best Local Similarity
                                                                                                 Query Match
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                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                             Human immunoglobulin polypeptide SEQ W0200155315-A2.
                                                                                                                                                                                                                                                                    Human ovarian specific polypeptide W02004013311-A2.
                                                                                                                                                                                                                                                                                                                                      Human ovarian specific polypeptide W02004013311-A2.
                                                                                                        02-AUG-2001.
(HUMA-) HUMAN GENOME
                                                                                                                           ABB10232 standard;
Human cDNA SEQ ID 1
WO200154474-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (LIUC/)
(ASUN/)
(CHEN/)
                                                   Human polypeptide
US2002090672-A1.
                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
ry Match 90.4%;
t Local Similarity 92.0%;
                                                                                                                                                                                            02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2003232054-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADH80722 standard; protein;
Human polypeptide #39.
                 (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C
                                                                       ABP66819 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DRMA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DOHZ)
                                                                                                                                                                                                                                                           (DIAD-) DIADEXUS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASUN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WANG/)
                                                                                                                                                                                                                                                                   2-FEB-2004.
                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                        ocal Similarity
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QIAN X B.
WANG Z W.
WEHRMAN T.
ZHANG J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TANG Y T.
LIU C.
ASUNDI V.
                                                                                                                                                                                                                                                                                                                                                                                                                                  CHEN R.
QIAN X B.
WANG Z W.
WEHRMAN T.
ZHANG J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZHOU P.
CAO Y.
                                                                                                                                                                                                                                                                                                                                                                                                                  ZHOU P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DRMANAC R
                                                                                                                                                                                                                                                                                                                                                                                                      DRMANAC R T.
Similarity
                                                                                                                                                                                                                                                                                                                                 DIADEXUS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASUNDI V.
                   G
                                                             ; protein; 301 AA.
SEQ ID NO 540.
                                                                                                                                     ; protein; 301
NO: 540.
                                                                                       SCI INC.
90.4%;
92.0%;
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97.1%;
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98.3%;
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                                                                                                                                                                                                                                                                                                                Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                      Score 1505;
Pred. No. 5.
                                                                                         Score 1396.5; DB Pred. No. 4.7e-94;
                                                                                                                                                                Score 1396.5;
Pred. No. 4.7e
                                                                                                                                                                                                                                         Score 1411;
Pred. No. 4
Score 1396.5; DB Pred. No. 4.7e-94;
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No. 1
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.6e-95;
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.5e-101;
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RESULT
ID AII
ID HO
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PN US
PD 11
PA (F
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PA (C)
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RESULT 405
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                                                              Query Match
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Best Local Similarity
ADH62550 standard; protein; 260 AA. Human PRO301 protein fragment #1. US2003171568-A1.
                                                                                                                                                                                                  AAY23326 standard;
An A33 related ant:
WO9927098-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY23328 standard; protein; 263 AA.
An A33 related antigen sequence.
W09927098-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JUN-1998.

(HOFF) HOFFMANN LA ROCHE & CO AG F.

(YMATCH 89.5%; Score 1382.5; DB /

"" ~ ~ 1 Similarity 91.0%; Pred. No. 4.9e-93;
                                                                                                               Human DNA40628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADR41522 standard; protein; 318 Human CD-like molecule HKACIO3, WO200226930-A2. 04-APR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADB31620 standard; protein; 301 AA Human novel protein SEQ ID NO 141. US2003077606-A1.
                                                                                                   WO9914241-A2.
                                                                                                                           AAY08072 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                         ADH62552 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human DNA40628 protein
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY08074 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human junctional adhesion molecule W09824897-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW61379 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
ry Match 90.4%;
t Local Similarity 92.0%;
                                                                         (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                               JS2003171568-A1.
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                                                                                                                                                                           GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                           TUMA/)
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                                                                                                                                                                                                                                                                                                                                                        ASHK/) ASHKENAZI A
                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                         GODDARD A.
) GURNEY A L.
) NAPIER M A.
) TUMAS D.
                                                                                                                                                                                                                                                                              00
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protein fragmen
                                                                                                             protein.
                                                                                                                                                                                                                ard; protein;
antigen seque
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88.9%;
Y 100.0%;
                                                87.8%;
100.0%;
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100.0%;
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100.0%;
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100.0%;
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92.0%;
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                                                                                                                                                                                                                 sequence.
                                                                                                                            260
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                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1372; pred. No. 2.
                                                                                                                                                  Score
Pred.
                                                                                                                                                                                                                           260 AA
                                                                                                                                                                                                                                                                                                                                                                                                        263 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1372;
Pred. No. 2.
                                                                                                                                                                                                                                                      Score 1372; DB 7;
Pred. No. 2.5e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
Pred.
                                                 Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                              #2.
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SEQ ID NO:321.
                                                1355;
. No. 4
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No. 5e-9
                                                                                                                                                   1355; DB 2;
. No. 4.3e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.5; DB
5e-94;
                                                 4.3e-91;
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.5e-92;
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.5e-92;
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Query Match
Best Local S
RESULT 411
RESULT
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Best Local Similarity
RESULT 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                      ADO08263 standard; protein;
Human NOVX polypeptide #5.
US2004018594-A1.
                                                                                                                                                                                                                                                                                                                                                      ABU69130 standard; protein; Human NOVX polypeptide #5. WO200290504-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human novel protein #40. WO200155437-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human JAM-1, F1: JP2004242513-A.
       (RIEG/
(SHEN/
(SHIM/
(SPYT/
                                              (MILL/)
(PADI/)
(PATT/)
(PENA/)
                                                                                                                                                                                                                                                                                                                                                                                                                             02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADR46575 standard; protein; 259 AA.
Human JAM-1, F11 receptor (F11R) transcript variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADQ95892 standard;
                                                                                                           (/TITT/)
(/TITT/)
                                                                                                                                                                                                                                 (ANDE/)
                                                                                                                                                                                                                                                              29-JAN-2004
                                                                                                                                                                                                                                                                                                                                              14-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU14169 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2004058805-A2.
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                                                                                                                                                                                (GERL,
                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH
ry Match 83.4%; Score 1287; DB 8;
Local Similarity 86.3%; Pred. No. 4.1e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ASAH-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ASHK/)
(FONG/)
                                                                                                                                        KEKU/
                                                                                                                                                   GUOX/
                                                                                                                                                            GUNT/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell activation
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                                                                                                                                                                                                                                                                                                               ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                              ocal Similarity
     MALYANKAR U M.
MALYANKAR U M.
MILLER C E.
MILLET I .
PADIGARU M.
PATTURAJAN M.
PENGA C E A.
RIRGER B K.
SHENOY S G.
SHIMKETS R A.
SPYTEK K A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GODDARD A.
GURNEY A L.
NAPIER M A.
TUMAS D.
WOOD W I.
                                                                                                                            GORMAN L.
GUNTHER E.
GUO X S.
KEKUDA R.
LEPLEY D M.
                                                                                                                                                                             ANDERSON D W.
BOLDOG F L.
BURGESS C E.
CASMAN S J.
CHAPOVAL A.
EDINGER S R.
GERLACH V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASAHI KASEI PHARMA CORP.
th 83.4%; Sco.
Similarity 86.3%; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASHKENAZI A. FONG S.
                                                                                                            LIU X.
                                                                                                                                                                                                                                                     ALSOBROOK J P.
                                                                                                                                                                                                                                                                                                                                    CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.8%;
100.0%;
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75.3%;
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86.0%;
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Pred.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1355;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein #35
                                                                                                                                                                                                                                                                                                                1114; DB 6;
No. 1.6e-73;
                                                                                                                                                                                                                                                                                                                                                                                               1281; DB 4;
No. 1.1e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.3e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 259;
                                                                                                                                                                                                                                                                                                                          Length 225;
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Best Local Similarity
RESULT 420
ID AAW74465 standard; pr
DE F11 antigen protein s
PN WO9902561-A1.
PD 21-JAN-1999.
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ID AID
DE MI
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PO 11
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(GETH ) GENENTECH INC.
(SETH) 69.5%; (
Match ---ity 68.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse junctional adhesion molecule-1, JP2004242513-A.
                                                                                                                                                                                                                                                                                                                                                 ADN35293 standard;
Human JAM protein.
WO2004031105-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine JAM protein US2003171568-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY23325 standard; protein;
A33 related antigen JAM.
                                                                                                                                                                                          Mouse junctional adhesion US2004235768-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US6699688-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADK40853 standard; protein; 300 AA.

Mouse junction adhesion molecule (JAM).
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Murine JAM protein used in 1
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(DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH
(S).9%; Score 1079.5; DB /
ry Match 69.9%; Pred. No. 7.5e-71;
                                                                                                                                                                                                                                  ADU66693 standard;
                                                                                                                                (KORN/) KORNECKI E.
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VOSS E
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NAPIER M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GODDARD A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASHKENAZI A.
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75.3%;
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68.1%;
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Score 1073.
Pred. No. 2
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No. 2.1e
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No. 1.
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No. 2.
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1.6e-73;
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2.1e-70;
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RESULT 424
                                 Query Match
Best Local Similarity
RESULT 429
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RESULT 426
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RESULT 423
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RESULT 422
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                                                                                                                                                                              AAU18030 standard; protein; 141 A Human immunoglobulin polypeptide W0200155315-A2.
                                                                                                                                                                                                                                                                         ABB72134 standard; protein; 134 AA. Human protein isolated from skin cells WO200190357-A1.
                                                                                                                                                                                                                                                                                                                                                                  AAB55934 standard;
Skin cell protein,
WO200069884-A2.
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Human platelet F11
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ABB10228 standard;
Human cDNA SEQ ID I
WO200154474-A2.
                                                                                                                                                                                                                                                                                                                                         (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY75995 standard; protein; 1
Human skin cell protein, SEQ
WO9955865-A1.
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25-NOV-2004.
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Human platelet F11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYNY) UNIV NEW YORK STATE RES FOUND.
ry Match 58.9%; Score 910;
t Local Similarity 97.2%; Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6699688-B1.
                                                                             02-AUG-2001
                                                                                        Human reproductive WO200155320-A2.
                                                                                                                AAM94741 standard;
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67.2%;
                                                                    (HUMA-) HUMAN GENOME
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                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
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          ; protein; 141
NO: 536.
                                                                                                   protein; 141 AJ
system related
                                                                                                                                                                                                                                                                                                                                                                              protein; 134 AA.
SEQ ID NO: 173.
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37.3%; Score 5
100.0%; Pred.
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                                                                                                                                                                                                                                                                                                                       37.3%;
100.0%;
                                           SCI INC.
34.0%;
100.0%;
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100.0%;
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98.5%;
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97.2%;
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Q ID
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                                            Score
Pred.
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Pred. No. 7.
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Pred. No. 1.
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                                               DB 4;
1.2e-30;
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2.1e-34;
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2.1e-34;
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.1e-58;
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1.2e-30;
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ID ADB316
DE Human
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PD 24-APF
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ID AI
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PD 03
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RESULT 433
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(MCCO/) MCCOY J M.

(LAVA/) LAVALLIE E R.

(COLL/) COLLINS-RACIE L

(EVAN/) EVANS C.

(MERB/) MERBERG D.

(TREA/) TREACY M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW85457 standard; protein; Secreted protein encoded by WO9842739-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                          Human junctional adhesion WO200114404-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human novel protein US2003077606-A1.
                                                                                                                                                                                           ABP61801 standard; protein;
Human polypeptide SEQ ID NO
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                                                                                                                                                                                                                                                                                                                                                                                      AAU00512 standard;
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(WEBE/) WEBER C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADW97861 standard; protein;
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Human polypeptide SEQ ID NO 536.
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ry Match 34.0%;
t Local Similarity 100.0%;
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CY Match 27.9%;
Local Similarity 35.3%;
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ry Match 34.0%;
Local Similarity 100.0%;
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n SEQ ID NO 175.
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                                                                                                                                                                                                                                                                                                                                                              protein; 298 AA.
hesion protein
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Pred. No. 2.2e-23;
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                                                                                                                                                                                                                                                        431; DB 4;
No. 2.2e-23;
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2.4e-26;
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1.2e-30;
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1.2e-30;
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1.2e-30;
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Query Match
Best Local Similarity
RESULT 438
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       (RUBE/) RUBEN S I
(ROSE/) ROSEN C I
(LIYY/) LI Y.
                                                                                                                                                                                                                                     AAE26983 standard; protein;
Human gene 25 encoded secret
US2002077287-A1.
                                                                                                                                                                                                                                                                                                            AAW75220 standard; protein; 298 AA. Human secreted protein encoded by g W09840483-A2.
                                                                                                                                                                                                                                                                                                                                                                                    ABM82288 standard; protein; Tumour-associated antigenic WC2004030615-A2.
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Human vascular endothelial junction-associated
                                           Human gene 25 en 
US2002076756-A1.
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TY Match 27.9%; Score

T Local Similarity 35.3%; Pred.
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ry Match 27.8%;
t Local Similarity 34.2%;
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                                    20-JUN-2002.
                                                              AAE27121 standard;
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) GREENE J M.
) FERRIE A M.
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WEI Y.
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ROSEN C
LI Y.
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KYAW H.
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RESULT 446
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RESULT 445
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(ROSE/) ROSEN C I
(LIYY/) LI Y.
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(ROSE/) ROSEN (RUBE/) RUBEN (LIYY/) LI Y.
                                                                                ADG89803 standard;
Human protein from
US2003225009-A1.
                                                                                                                                                                                                          08-MAY-2003.
(HUMA-) HUMAN GENOME
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                                                                                                                                                                                                                                                                           ADC74331 standard; protein; 298 AA.
Human secreted protein - SEQ ID 964
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADB91670 standard; protein; 298 AA.
Human secreted protein #SEQ ID 616.
                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003004622-A2.
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ry Match 27.8%;
t Local Similarity 34.2%;
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ry Match 27.8%;
Local Similarity 34.2%;
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KYAW H.
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WEI Y.
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3.1e-23;
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                                                                      AAM93905 standard;
Human polypeptide,
EP1130094-A2.
                                                                                                                                                                                                                                                                                                                    Human PRO1868 protein UNQ859 WO200053758-A2
                                                                                                                                                                                                                                                                                                                                                                                                    PRO1868, an A33 antigen homologue.
WO200036102-A2.
AAM93323 standard;
Human polypeptide,
                                                 (HELI-) HELIX RES
                                                                                                                                                    Human PRO1868 p
WO200104311-A1.
                                                                                                                                                                         AAB80272 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                         AAY96735 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human junctional WO2003008541-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAO16453 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAO16452 standard;
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(KYAW/)
(FISC/)
(LIHH/)
                                                                                                                                                                                                                  (RMFD-) RMF DICTAGENE
                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                           AAB33457 standard; protein;
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-2001. INC.

) GENENTECH INC.

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FERRIE A M.
HASTINGS G
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27.5%;
h 27.5%;
Similarity 32.8%;
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                                                                                                                                                               protein.
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adhesion molecule 3
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                            3 INST.
27.5%;
32.8%;
protein; 310 AA
SEQ ID NO: 2845
                                                                              protein; 310 AA.
SEQ ID NO: 4051.
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No. 7.
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No. 7.5e-23;
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No. 7.5e-23;
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No. 4.5e-23;
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No. 3.6e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human PRO1868 polypeptide sequence. WO200140466-A2.
                                                                                                                                                                                                                                                                                                                                                          ABG92709 standard; protein; 310 Human secreted protein PRO1868. US2002098506-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Secreted protein WO200107459-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB80383 standard; protein; 310 A
secreted protein encoded by gene
Human albumin
WO200177137-A1
                                                                                      Human albumin fusion WO200177137-A1.
                                                                                               ABG65297 standard; protein; 310 AA.
Human albumin fusion protein #1972.
                                                                                                                                                                                                                                                                              ABG91361 standard; provel human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB80409 standard; protein; 310 AA. Secreted protein encoded by gene #39.
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(HELI-) HELIX RES
                                                               18-OCT-2001.
(HUMA-) HUMAN GENOME
                                                                                                                                                                                        Human PRO1868 protein
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(HUMA-) HUMAN GENOME SCI INC.
                    ABG65296 standard;
                                                                                                                                                                             WO200200690-A2.
                                                                                                                                                                                                   ABB84947 standard;
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ry Match 27.5%;
Local Similarity 32.8%;
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(HUMA-) HUMAN GENOME
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                                Local Similarity
467
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) GENENTECH INC.
27.5%; 5
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27.5%;
Y 32.8%;
         protein; 310 AA.
on protein #1971.
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27.5%;
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Pred. No. 7.5e-23;
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Pred. No. 7.
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No. 7.5e-23;
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No. 7.5e-23;
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7.5e-23;
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RESULT 468
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(HUMA-) HUMAN GENOME
                ABO17884 standard;
Novel human secret
US2003032156-A1.
                                                                                   US2002192668-A1.
                                                                                                                                                    ABU72377 standard; protein; 310 AA.
Novel human secreted and transmembrane
US2002182618-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                      Human angiogenesis WO200208284-A2.
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Human angiogenesis related p
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Human PRO1868 polypeptide.
US2002098507-A1.
                                                                                            Human secreted and
                                                                                                    ABU80867 standard;
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) GENENTECH INC.

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STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
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GODOWSKI P J.
GURNEY A L.
HILLAN K J.
MARSTERS S A.
                                                           GENENTECH INC.
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GENENTECH INC.
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GENENTECH INC
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RESULT 475
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RESULT 476
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26-DEC-2002.
(GETH) GENENTECH INC.
(GETH) GENENTECH 27.5%; (
MARICH 27.5%; (
MARICH 32.8%;
                         Human PRO polypeptide #269.
US2003036180-Al.
20-FEB-2003.
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                                                                                                                       Novel human secreted and transmembrane US2002197671-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein #592. W02002102994-A2.
                                                                                                                                                                                                                      Human secreted/transmembrane US2003003530-A1.
                                                                                                                                                                                                                                            ABU71951 standard; protein; 310 AA.
                                                                                                                                                                                                                                                                                                             ABU81138 standard; protein; 310 AA Human PRO polypeptide #269. US2003004311-A1.
                                                                                                                                                                                                                                                                                                                                                                                                      WO2003006673-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                ABP71277 standard; protein; 310 AA. Human junctional adhesion molecule
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADA57309 standard; protein;
Human secreted protein #592.
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WO2002102994-A2.
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ry Match 27.5%;
t Local Similarity 32.8%;
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ry Match 27.5%; Score
Local Similarity 32.8%; Pred
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27.8%;
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19-SEP-2002.
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27-5%; (Match 27-5%; (
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20-FEB-2003.
(GETH ) GENENTECH INC.
27.5%; (
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23-JAN-2003.
(GETH ) GENENTECH INC.
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45.Ch 27.5%;
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06-MAR-2003.

(GETH ) GENENTECH INC.

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27.8%;
                                         ABU60813 standard; protein; Human secreted/transmembrane US2002160392-A1.
                                                                                                                      Human secreted / US2003036060-A1. 20-FEB-2003.
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                                                                                                                                                                                                              US2003023054-A1.
30-JAN-2003.
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Human secreted protein PRO1868.
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31-OCT-2002.
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Human secreted/transmembrane
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Novel secreted and
US2003017563-A1.
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                                                                                                              (GETH
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US2002164646-A1.
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US2003017463-A1.
23-JAN-2007
                                             Homo sapiens.
US2003049816-A1.
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Human PRO polypeptide #269.
US2003054517-A1.
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Human PRO polypeptide #269.
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US2003032060-A1.
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17-APR-2003.
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Novel human secreted and transmembrane
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US2003082704-A1.
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Human PRO polypeptide #269.
US2003068795-A1.
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Human PRO polypeptide #269.
US2003087350-A1.
                                                        ADB30718 standard; protein;
Human PRO polypeptide #269.
US2003068794-A1.
                                                                                                                                                                                                                   ABO32816 standard; protein; 3 Human secreted/transmembrane US2003045693-A1.
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Human secreted/transmembrane
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US2003073215-A1.
ADA86014 standard; protein;
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US2003077721-A1.
24-APR-2003.
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US20030B2703-A1.
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US2003064367-A1.
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RESULT 539
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22-MAY-2003.
(GETH ) GENENTECH INC.
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15-MAY-2003.
(GETH) GENENTECH INC.
27.5%;
Match 27.5%;
Human PRO polypeptide #269.
US2003082760-A1.
01-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human PRO polypeptide #269. US2003082702-A1.
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                                                                                                                                                                                                                                                                                                                       ADA96122 standard;
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(GETH ) GEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADA96674 standard; protein;
Human PRO polypeptide #269.
US2003082690-A1.
01-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADB24345 standard; protein; 310 Human PRO polypeptide SEQ ID NO US2003077714-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU62957 standard; protein;
Human PRO1868 protein.
US2003054447-A1.
20-MAR-2003.
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Human PRO polypeptide #269.
US2003096386-Al.
22-MAY-2003.
                                                                                                                                                                                                           (GETH )
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US2003049817-A1.
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Best Local Similarity RESULT 555
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13-MAR-2003.
(GETH ) GENENTECH INC.
27.5%; (MARCH 27.5%; (MARCH 27.5%; (MARCH 27.5%); 
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01-MAY-2003.
(GETH ) GENENTECH INC.
27.5%;
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OI-MAY-2003.

(GETH ) GENENTECH INC.

27.5%; (
Watch '17/(ty 32.8%;
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10-APR-2003.
(GETH ) GENENTECH INC.
27.5%; (
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US2003082765-Al.
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                                                                                                          ADA46609 standard; protein; Novel human secreted and trauscommon us2003054516-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted/transmembrane US2003082540-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA13312 standard; protein; 310 AA. Human secreted/transmembrane protein, US2003049622-A1.
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Human PRO polypeptide #269.
US2003077710-A1.
                                                                                                                                                                                                                                                                                                                                                      ADA88221 standard; protein; 310 AA. Novel human secreted and transmembrane US2003082700-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2003082709-A1.
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Novel human secreted and tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA42180 standard; protein;
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-2003.
) GENENTECH INC.
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-4 ty 32.8%;
                                                        GENENTECH
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.5e-23;
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.5e-23;
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RESULT 565
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RESULT 563
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Best Local Similarity
RESULT 561
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Best Local Similarity
RESULT 560
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          Query Match
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US2003059909-A1.
27-MAR-2003
                                ADB27535 standard; protein;
Human PRO polypeptide #269.
US2003022239-A1.
                                                                                                                    ADA97778 standard; protein;
Human PRO polypeptide #269.
US2003082686-A1.
                                                                                                                                                                                                                                                                                                                                                                                           ABO01894 standard; protein; Novel human secreted and traus2003027256-A1.
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US2003082699-A1.
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                      30-JAN-2003.
                                                                                                              01-MAY-2003
                                                                                                                                                                                                                        Novel human secreted and transmembrane
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                                                                                                 (GETH ) GENENTECH INC.
                                                                                                                                                                                         (GETH
                                                                                                                                                                                                            US2003073213-A1.
                                                                                                                                                                                                                                  ADA88773 standard; protein; 310 AA
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                                                                                                                                                                                                                                                                                                                                                                      (GETH
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Human secreted/transmembrane US2003036061-A1.
                                                                                ADC40445 standard; protein; i Human secreted/transmembrane US2003059829-A1.
                                                                                                                                                                  ADC39931 standard; protein; i Human secreted/transmembrane US2003059828-A1.
                                                                                                                                                                                                                                                    ADC28731 standard; protein; 310 AA. Human secreted/transmembrane protei US2003059772-A1.
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Human PRO polypeptide SEQ ID NO 538
US2003077720-A1.
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                    T 593
ADC19269 standard;
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Human secreted/transmembrane
US2003036094-A1.
                                                                                                                                                                                Human PRO1868 protein, US2003077657-A1.
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                                    ADC50579 standard; protein; Novel human secreted and traUS2003092106-A1.
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                        ADC53718 standard; protein; 310 AA. Novel human secreted and transmembrus2003087364-A1.
                                                                                                       ADC54757 standard; protein; 310 AA. Novel human secreted and transmembrane
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Human PRO polypeptide #269.
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Human secreted protein - SEQ
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(GETH ) GENENTECH INC.
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                                  ADD05222 standard; protein; Human secreted/transmembrane US2003104469-A1.
                                                                                                               ADC48111 standard; protein;
Human PRO polypeptide #269.
US2003194771-A1.
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Best Local Similarity RESULT 638
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Best Local Similarity
RESULT 636
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Best Local Similarity
RESULT 635
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Best Local Similarity
RESULT 634
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                                                              Query Match
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US2003194769-Al.
16-OCT-2003.
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US2003203438-A1.
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                                                                                                                      ADD53784 standard; protein; 310 AA. Novel human secreted and transmembr US2003203437-A1.
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Human secreted/transmembrane
US2003104381-A1.
05-JUN-2003.
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Human secreted/transmembrane
US2003105013-A1.
05-JUN-2003.
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ADD37304 standard; protein;
                                                                                   (GETH
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Human PRO polypeptide #269.
US2003199030-A1.
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US2003203430-A1.
30-OCT-200
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US2003203431-A1.
30-OCT-2009
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Novel human secreted and transmembrane
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Human PRO polypeptide #269.
US2003194779-Al.
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Human secreted protein #192.
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ADD91568 standard; protein;
Human PRO polypeptide #269.
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ry Match 27.5%;
t Local Similarity 32.8%;
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WO200290526-A2.
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Best Local Similarity RESULT 657
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23-OCT-2003
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Human PRO polypeptide #269.
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Human PRO polypeptide #269.
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Human PRO polypeptide #269.
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23-OCT-2003.
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Human PRO polypeptide #269.
US2003194772-A1.
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ADE34135 standard; protein; Novel human secreted and traUS2003194791-A1.
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23-OCT-2003.
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Human PRO polypeptide #269.
US2003199026-A1.
23-OCT-2003.
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16-OCT-2003.
(GETH) GENENTECH INC.
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(GETH) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.

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(GETH ) GENENTECH INC.
(GETH ) 27.5%;
                                                                                              ADG21688 standard; protein; 310 AA Novel human secreted and transmembs US2003207355-A1.
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                                                                         06-NOV-2003.
(GETH ) GENENTECH INC.
         ADG23329 standard; protein; 310 Novel human secreted and transme US2003207384-A1.
                                                                                                                                                                           ADE92979 standard; protein;
Human PRO polypeptide #269.
US2003194777-A1.
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Human PRO polypeptide #269.
US2003199034-A1.
23-OCT-2003.
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Human PRO polypeptide #269.
US2003199031-A1.
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Human PRO polypeptide #269.
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Novel human secreted and transmembrane
US2003207379-A1.
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Human PRO polypeptide #269.
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(GETH ) GENENTECH
                                                       ADI38318 standard; protein; 310 AA. Human secreted/transmembrane protein,
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Human PRO polypeptide #269.
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US2003087355-A1.
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(GETH) GENENTECH INC.
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30-OCT-2003.
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US2003100087-A1.
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US2003092115-A1.
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US2003203439-A1.
30-OCT-2003.
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Human PRO polypeptide #269.
US2003092111-A1.
15-MAY-2003.
ADE18540 standard; protein;
Human PRO polypeptide #269.
US2003194794-A1.
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US2003092110-A1.
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US2003092108-A1.
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ADE92427 standard; protein; 310 AA. Novel human secreted and transmemby US20031990:1-A1.
23-OCT-2003.
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Human PRO polypeptide #269.
US2003199029-A1.
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Human PRO polypeptide #269.
US2003199061-A1.
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Human secreted/transmembrane protein,
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                                                                                                      ADE98809 standard; protein;
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Human secreted/transmembrane
US2003180312-A1.
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Human secreted/transmembrane protein,
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                                  ADF73676 standard; protein; i
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US2003207371-A1.
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Human PRO polypeptide #269.
US2003207374-A1.
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US2003207423-A1.
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US2003207390-A1
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US2003207363-A1.
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RESULT 774
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(GETH ) GENERITECH INC.

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US2003194793-A1.
16-OCT-2003.
                                                                                                                                                                                                                                                                                                                                    Novel human secreted and transmembrane US2003207367-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADH12785 standard; protein; Novel human secreted and traus2003207378-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADH28718 standard; protein;
Human PRO polypeptide #269.
US2003022331-A1.
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                                    Human secreted/transmembrane US2004005553-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADG56519 standard; protein; 310 AA. Novel human secreted and transmembr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2003207416-A1.
                                                                            ADH20735 standard;
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(GETH ) GENENTECH INC.
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Match 27.5%;
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US2003207361-A1.
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US2003148419-A1.
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ADI37884 standard; protein; 310 AA.
Human secreted/transmembrane protein,
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GODOWSKI P J.
GURNEY A L.
MATHER J P.
MILLIAMS P M.
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MATHER J P.
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GODDARD A.
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Novel human secreted and transmembrane
US2003207383-A1.
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(GETH ) GENENTECH INC.
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US2003228664-A1
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              ADL78564 standard; protein; 310 Albumin fusion protein related t US2004010134-Al.
                                                                                           ADL78563 standard; protein; Albumin fusion protein relat US2004010134-A1.
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Human secreted/transmembrane
US2003190611-A1.
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(GETH ) GENENTECH INC.
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Human PRO polypeptide #60. US6686451-B1. 03-FEB-2004.
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US200403836-Al.
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Human PRO polypeptide #269.
US2004038335-A1.
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Human PRO polypeptide #131.
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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ry Match 27.5%;
t Local Similarity 32.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADL78565 standard; protein; 310 AA. Albumin fusion protein related therapeutic US2004010134-A1.
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(REAS-) RES ASSOC BIOTECHNOLOGY.

27.5%; Score

t Local Similarity 32.8%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ROSE/) ROSEN C A.
(HASE/) HASELTINE W A.
                                                                      GETH ) GENENTECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocal Similarity
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                                   A INC.
27.5%
32.8%;
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full length
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.5e-23;
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.5e-23;
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Best Local Similarity
RESULT 814
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RESULT 813
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RESULT 811
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22-APR-2004.

(GETH) GENENTECH INC.

27.5%;

MATCH 27.5%;

27.5%;
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15-APR-2004.
(GETH) GENENTECH INC.
(GETH) 27.5%;
MATCH 27.5%;
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                                                                                                                                                                                           ADR11310 standard; protein; 
Human secreted/transmembrane
US2004137561-A1.
                                                                                                                                                                                                                                                                              ADP69035 standard; protein; Human NOV2f protein SEQ ID NWC2004055158-A2.
                                                                                                                                                                                                                                                          01-JUL-2004.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                   ADP69033 standard; protein; Human NOV2e protein SEQ ID 1 WO2004055158-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-2004.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADP69025 standard; protein; Human NOV2a protein SEQ ID N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADP69027 standard; protein; 310 AA.
Human NOV2b protein SEQ ID NO:22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human PRO1868 protein. WO2004031105-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADN35310 standard;
                                                                       (ASHK/)
(BOTS/)
                                                                                                        US2004147017-A1.
                                                                                                                  Human secreted/transmembrane
                                                                                                                            ADR18219 standard; protein; 310 AA
                                                                                                                                                                       (GETH
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                             DESNOYERS L.
EATON D L.
FERRARA N.
FILVAROFF E.
                                                                                                                                                 Similarity
                                                                                                                                                                      GENENTECH INC.
GERBER H.
                     FONG
                                                                       ASHKENAZI A.
BOTSTEIN D.
                    <u>د</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein;
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32.8%;
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NO:30.
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Query
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Best Local Similarity
RESULT 820
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24-APR-2003.
(GETH ) GENENTECH INC.
27.5%; (
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(ROYM/) ROY M A.
(STEW/) STEWART T A.
(TUMA/) TUWAS D M.
(WILL/) WILLIAMS P M.
(WOOD/) WOOD W I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ASHK/) ASHKENAZI A.
(BOTS/) BOTSTEIN D.
(DESN/) DESNOYERS L.
(EATO/) EATON D L.
(FERR/) FERRARA N.
(FILV/) FILMAROFF E.
                                                            ADS32474 standard; protein; 310 AA. Novel human secreted and transmembrane US2004203125-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADI96522 standard; protein; 310 AA. Novel human secreted and transmembrane
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US2003077659-A1.
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                                           (GETH )
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GODOWSKI P J.
GRIMALDI C J.
GURNEY A L.
HILLAN K J.
KLJAVIN I J.
                                                                                                                                                                                                                                                                                            PAONI N F.
                                         GENENTECH INC
                                                                                                                                                                                                         WOOD W I.
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GODDARD A.
Similarity
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TUMAS D.
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MATHER J E
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                                                                                                                                                                                                                                                                                                                                                                                               GURNEY A L.
HILLAN K J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GERRITSEN M E.
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GRIMALDI C J.
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32.8%;
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32.8%;
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Pred. No. 7.5e-23;
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No. 7.
  424; DB 8;
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No. 7.5e-23;
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                   Length 310;
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Best Local Similarity
RESULT 825
ID AEB14255 standard; p.
DE Cancer cell diagnosi;
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BARE/) BARER K P.
PA (BERE/) BERESINI M.
PA (DESO/) DEFORGE L.
PA (DESO/) DEFORGE L.
PA (FILV/) FILVAROFF E.
PA (GADOW/) GAO W.
PA (GADOW/) GAO W.
PA (GODD/) GODDARD A.
PA (GODD/) GODDARD A.
PA (GODN/) GODDARD A.
PA (GONN/) GURNEY A L.
PA (STEW/) STEWART T A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABB C K
PA (WOOD/) WATANABB C K
PA (WOOD/) WATANABB C K
                                                                                                                                                                                                 Query Match
Best Local S
RESULT 826
                                                                                                     RESULT 827
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Best Local Similarity
RESULT 824
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            Best Loca
RESULT 828
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US2004214269-A1.
28-OCT-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEA38133 standard; protein; Human secreted/transmembrane US2005112725-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADT03895 standard; protein; 310 Human secreted/transmembrane pro US2003152922-A1.
                                                                   AAB38384 standard; protein; 311 AA. Human secreted protein encoded by g WO200061623-A1.
                                                                                                                                                             AAB38383 standard; protein; 311 AA. Human secreted protein encoded by g W0200061623-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEB14255 standard; protein; 310 AA. Cancer cell diagnosis method-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-APR-2005
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AAB38333 standard; protein; 311 AA.
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                                                                                                                                                                                                                                   (ZHAN/)
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-2004.
) GENENTECH INC.
27.5%; 5
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BERESINI M.
DEFORGE L.
DESNOYERS L.
FILVAROFF E.
                                                                                                                                                                                                                                                                                                   GODDARD A.
GODOWSKI P J.
GURNEY A L.
SHERWOOD S.
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                                              HUMAN GENOME
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                                                                                                                                                                                                                                                                               SMITH V.
STEWART T A.
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27.5%;
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Pred. No. 7.5e-23;
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7.5e-23;
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.5e-23;
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RESULT 830
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RESULT 831
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                                                                                                                                      Human confluency regulated & WO200053749-A2.
14-SEP->nnn
                                                                                                                                                                                                                                                                                                                                                                              Human junction adhesion molecule 3 WO2004053058-A2.
                                                                                                                                                                                                                            AAB27278 standard;
Murine confluency 1
WO200053749-A2.
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Gene #13 associated
WO200107459-A1.
                                                                            Human F11-adhesion
                                                                                                                          (RMFD-) RMF DICTAGENE
                                                                                                                                                                                                                                                                                                          Human EST encoded protein SEQ ID NO: WO200154477-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human IGFAM-6 immunoglobulin.
WO200029583-A2.
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                                                                   US6699688-B1.
                                                                                      ADK40850 standard;
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26.7%; Score 412
C2-type Ig
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regulated
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protein;
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No. 8
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No. 3.
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8e-23;
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1.1e-22;
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RESULT 842
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RESULT 845
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RESULT 839
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25-MAR-1999.
(GETH ) GENENTECH INC.
26.2%; (Match 'lavity 35.2%;
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03-101-1999.

(GETH) GENENTECH INC.

26.2%

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(GETH ) GENENTECH INC.
(BETH) 26.2%;
Match 25.2%;
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Human FAM C2-type Ig
US2004235768-A1.
25-NOV-2004.
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WO9914241-A2.
25-MAR-1999.
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                                                                                                                                   AAB33421 standard;
Human PRO245 protei
WO200053758-A2.
                                                                                                                                                                                                                                                                                                                                                                       AAY23324 standard; protein; A33 related antigen PRO245. WO9927098-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYNY ) UNIV NEW YORK STATE | 2ry Match 26.5%; t Local Similarity 100.0%;
                                                                 AAY70668 standard; protein;
Human PRO245 protein.
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02-MAR-2004
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Human F11-adhesion molecule
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Human secreted protein sequence
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25-NOV-2004.
AAB24401 standard; protein;
                                      (GETH ) GENENTECH INC.
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WO9914328-A2.
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                                                        numan PKO245 protein.
NO200015797-A2.
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H ) GENENTECH INC.
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SOBOCKA M B.
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of protein PRO245.
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Best Local :
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Human PRO polypeptide #11.
US2002192659-A1.
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US2002146709-A1.
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Human PRO245 protein.
WO200015796-A2.
                                                                                                                                                                                                                                                                                                                                                                                  AAU12339 standard;
Human PRO245 polype
WO200140466-A2.
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WO200104311-A1.
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WO200032221-A2.
                                                                                                                                                        ABO17783 standard; protein; 312 AA.
Novel human secreted and transmembr
ABU81037 standard; protein;
Human PRO polypeptide #168.
                                                                                                                                                JS2003032156-A1.
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polypeptide seq
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ABU67355 standard; protein; 312 Human secreted protein PRO245. US2003023054-A1.
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Human secreted/transmembrane protei
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US2003003530-A1.
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(GETH ) GENENTECH INC.
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Human PRO polypeptide #168. US2003054517-A1.
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Novel human secreted and transmembrane
US2003017463-A1.
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Human PRO polypeptide #168. US2003068795-A1.
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Human secreted/transmembrane
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Human PRO polypeptide #168.
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Human PRO polypeptide #168.
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Best Local Similarity RESULT 908
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(GETH ) GENENTECH INC.

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US2003073210-A1.
17-APR-วกกำ
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US2003082703-Al.
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Novel human secreted and transmembrane
US2003082695-A1.
01-MAY-2003
(GETH ) GENENTECH INC.
(GETH ) GENENTECH INC.
1t Local Similarity 35.2%; Pred. No.
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(GETH) GENENTECH INC.

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24-APR-2003.
(GETH ) GENENTECH INC.
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(GETH ) 26.2%;
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US2003082702-A1.
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                                                          ADA95920 standard; protein; Human PRO polypeptide #168.
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Human PRO polypeptide #168.
US2003096386-A1.
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Human PRO polypeptide #168.
US2003077721-A1.
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Human PRO polypeptide SEQ ID US2003077715-A1.
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US2003049817-A1.
ADB26229 standard; protein;
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(GETH ) GENENTECH INC.
(GETH ) 26.2%;
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US2003082709-A1.
01-MAY-2007
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US2003068797-A1.
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                                                             ADA88019 standard; protein; 312 AA.
Novel human secreted and transmembrane
US2003082700-A1.
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Novel
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       ADA46407 standard;
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US2003049622-A1.
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US2003082686-A1.
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                                                                          ADB27333 standard; protein;
Human PRO polypeptide #168.
US2003022239-A1.
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Human secreted/transmembrane
US2003054351-A1.
20-MAR-2003.
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08-MAY-2003.

(GETH ) GENENTECH INC.

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(GETH ) GENENTECH INC.
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US2003087352-A1.
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US2003082689-A1.
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Human PRO polypeptide SEQ ID
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Human PRO polypeptide #168.
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Human PRO polypeptide #168.
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Novel human secreted and transmembrane
US2003082764-A1.
                                       ADB34453 standard; protein;
Human PRO polypeptide SEQ II
US2003077717-A1.
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(GETH ) GENENTECH INC.
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Human PRO polypeptide #168.
US2003082762-A1.
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Human PRO polypeptide #168.
US2003082698-A1.
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DE Human PRO polypeptid
PN US2003077716-A1.
PD 24-APR-2003.
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ID ADC400
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                           Human secreted/transmembrane US2003036061-A1.
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                                                              ADC71924 standard; protein; 312 AA.
Novel human secreted and transmembrane
US2003092107-A1.
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Novel human secreted and transmembrane
US2003092106-A1.
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Human secreted/transmembrane
US2003073079-A1.
17-APR-2003.
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Human secreted/transmembrane 
US2003054400-A1.
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Human secreted/transmembrane
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RESULT 977
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ID ADC572
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RESULT 983
ID ADC55917 standard;
DE Novel human secrete
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Novel human secreted and tra
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                                                                   US2003087359-A1.
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Novel human secreted
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US2003087362-A1.
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Novel human secreted and transmembrane
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US2003087354-A1.
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Human PRO polypeptide #168.
US2003194773-A1.
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ry cocal Similarity 35.
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08-MAY-2003.
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ADC80521 standard; protein; 312 AA.
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(GETH ) GENENTECH INC.
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Human PRO polypeptide #168.
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US2003199055-A1.
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Human PRO polypeptide #168. US2003199057-A1.
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Human PRO polypeptide #168.
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Human PRO polypeptide #168.
US2003203431-A1.
30-OCT-2003.
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Human PRO polypeptide #168.
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Human PRO polypeptide #168.
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Best Local Similarity
RESULT 1055
ID ADI63485 standard; p
DE Novel human secreted
PN US2003207387-A1.
PD 06-NOV-2003.
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Best Local Similarity
RESULT 1047
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08-MAY-2003.

(GETH ) GENENTECH INC.

26.2%; (

14-10 25.2%; (

14-10 35.2%;
                                                                                                                                                                      Novel human secreted and transmembrane US2003087357-A1.
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   Novel human secreted and tra
US2003207387-A1.
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Novel human secreted and tra
US2003087355-A1.
08-MAY-2003.
                                                                                    Novel human secreted and transmembrane US2003207385-A1.
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Novel human secreted and transmembrane
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20-MAR-2003.
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Human secreted/transmembrane protein,
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Novel human secreted and transmembrane
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Best Local Similarity
RESULT 1064
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15-MAY-2003.
(GETH ) GENENTECH INC.
(GETH ) 26.2%;
March 26.2%;
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US2003211571-A1.
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Human PRO polypeptide #168.
US2003092108-A1.
15-MAY-2002
                                                                          ADE73242 standard; protein; 3
Human secreted/transmembrane
US2003129592-A1.
10-JUL-2003.
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Human PRO polypeptide #168.
US2003203440-A1.
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Human PRO polypeptide #168.
US2003092113-A1.
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Human PRO polypeptide #168.
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H) GENENTECH INC.

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LOCAL Similarity

RESULT 1071

ID ADE88647 stand*

DE Human PRO r

PN US20031°

PD 23-0

PA 23-0
                                                                                      Best Local Similarity
RESULT 1072
ID ADE99331 standard, p
DE Human secreted/trans
PN US2003211576-A1.
PD 13-NOV-2003
PA (GETH ) GENENTECH IN
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ID ADE8919
DE Human Pl
PN US20031
PD 23-OCT--
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US2003199062-A1.
23-OCT 2003.
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US2003203439-A1.
                             ADE94667 standard; protein;
Human PRO polypeptide #168.
US2003199027-A1.
                                                                                                         ADE99331 standard; protein; 312 AA Human secreted/transmembrane proteins US2003211576-A1.
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US2003199054-A1.
23-OCT->>or
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US2003092111-A1.
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(GETH ) GENENTECH
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US2003199058-A1.
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Novel human secreted and transmembrane
US2003199051-A1.
23-OCT-2003.
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Human PRO polypeptide #168.
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(GODD/) GODDARD A.
(GODD/) GODWSKI P J.
(GURN/) GURNEY A L.
(MATH/) MATHER J P.
(MILL/) MILLIAMS P M.
(MODD/) MODD W I.
                                                       Human PRO polypeptide #168.
US2003208055-Al.
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US2003207376-A1.
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US2003207352-Al.
06-NOV-2007
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Human secreted/transmembrane
US2003180312-A1.
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06-NOV-2003.

(OSTH) GENENTECH INC.

26.2%; (

Match 26.2%; (

35.2%;
Human PRO polypeptide #168.
US2003207371-A1.
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US2003207424-A1.
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Human secreted/transmembrane
US2003166051-A1.
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Human PRO polypeptide #168.
US2003207359-A1.
06-NOV-2003.
                                                                                       ADG15512 standard; protein;
Human PRO polypeptide #168.
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(GETH ) GENENTECH INC.
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Human PRO polypeptide #168.
US2003207357-A1.
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Human PRO polypeptide #168.
US2003207375-A1.
06-NOV-2003.
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Human PRO polypeptide #168.
US2003207353-A1.
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06-NOV-2003.
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US2003207356-A1.
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06-NOV-2003.
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Novel human secreted and transmembrane
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Human PRO polypeptide #168.
US2003207358-A1.
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                                                                                           Human secreted/transmembrane US2003027146-A1.
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Novel human secreted and transmembrane
US2003207362-A1.
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Novel human secreted and tra
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                US2003207363-A1.
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Best Local Similarity
RESULT 1127
ID ADG56317 standard; p
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PN US2003207366-A1.
PD 06-NOV-2003
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(GETH ) GENENTECH INC.
(GETH ) 26.2%; (
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US2003207414-A1.
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Human secreted/transmembrane protein,
                           US2004009547-A1.
15-JAN-2004.
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(WILL/) WILLIAMS P M.
(WOOD/) WOOD W I.
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Best Local Similarity
RESULT 1161
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Best Local Similarity
RESULT 1159
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Human secreted/transmembrane protein, #:
US2004147017-A1.
29-JUL-2004.
(ASHK/) ASHKENAZI A.
(BOTS/) BOTSTEIN D.
(BOTS/) DESNOYERS L.
(LETO/) EATON D L.
(FERR/) FERRARA N.
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11-MAR-2004.
(GETH ) GENENTECH INC.
26.2%; 5
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US2004058424-A1.
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US200403836-A1.
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US2004077064-A1.
22-App----
                                                                                                                                                                                                                                                                                             Human PRO245 protein, WO2004031105-A2.
                                                                                                                                                                                                                                                                                                                                                             ADO06099 standard; protein;
Human PRO polypeptide #11.
US6686451-B1.
03-PEB-2004.
(GETH) GENENTECH INC.
                                                                                                                                        ADR10951 standard; protein; Human secreted/transmembrane US2004137561-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADM27700 standard; protein;
Human PRO polypeptide #168.
US2004048333-A1.
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Human PRO polypeptide #168.
US2004038335-A1.
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                                                                             ADR17860 standard; protein; 312 AA
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RESULT 1164
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AU2003259607-A1.
27-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                               ADI96320 standard; protein; 312 AA.
Novel human secreted and transmembrane
US2003207354-A1.
                                                                                                                                Human secreted/transmembrane protein US2004185531-A1.
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Human PRO polypeptide #168.
US2003077659-A1.
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(FONG/)
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(DESN/)
(EATO/)
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H) GENENTECH INC.
26.2%; //
GERRITSEN M E.
GODDARD A.
GODOWSKI P J.
GRIMALDI C J.
GURNEY A L.
HILLAN K J.
                                                                        ASHKENAZI A.
BOTSTEIN D.
DESNOYERS L.
EATON D L.
FERRARA N.
FILVAROFF E.
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GODDARD A.
GODOWSKI P J.
GRIMALDI C J.
GURNEY A L.
HILLAN K J.
KLJAVIN I J.
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STEWART T A.
TUMAS D.
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Best Local Similarity
RESULT 1168
ID ADT03256 standard; F
DE Human PRO polypeptic
PN US2004214269-A1.
PD 28-OCT-2004.
RESULT 1170
ID ADZ0330
DE Human s
PN US20050
PD 07-APR-
PA (GETH)
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                                                                                                                 (BAKE/) BAKER K P.
(BERE/) BEFOSINI M.
(DEFO/) DEFORGE L.
(DESN/) DESNOYERS L.
(FILV/) FILVAROFF B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADT03256 standard; protein; 312 AA Human PRO polypeptide #168. US2004214269-A1.
                                                                                                                                                                                                                                                                                                                                   ADZ03307 standard; protein; 312 AA Human secreted/transmembrane PRO24: US2005074837-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                ADT03536 standard; protein; 312 AA Human secreted/transmembrane proteins2003152922-A1.
                                                                                                                                                                           AEB14053 standard; protein; 312 AA. Cancer cell diagnosis method-related US2005153396-A1.
                                                                                                                                                                                                                                                                  Human secreted/transmembrane
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) GENENTECH INC.
26.2%; (
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GODDARD A.
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MATHER J P.
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ROY M A.
STEWART T A.
                                                         GURNEY A L. SHERWOOD S.
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           WATANABE C K.
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                                                                                                           ABB06037 standard; protein; Human NS protein sequence S WO200206315-A2.
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                            ABG22341 standard; protein; 388 Novel human diagnostic protein WO200175067-A2.
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Human confluency regulated
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        11-OCT-2001.
(HYSE-) HYSEQ
                                                                                                    24-JAN-2002
                                                                                                                                                                         (RMFD-) RMF DICTAGENE SA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB70500 standard; protein; 215 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human PRO245 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB50904 standard; protein;
                                                                                                                                                                                                                  AAB27275 standard; protein;
                                                                                                                                                                                                                                                          14-SEP-2000
(RMFD-) RMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUL-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM41947 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200073452-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                          (EOSB-)
                                                                                                                                                                                                                                                                                                                                                                                                                                   15-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH )
                                                                                                                                                                                                                                                                                                                                                                                                   ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3454
-2000.
) GENENTECH INC.
26.0%; f
                                                                                                                                                                                                                                    RMF DICTAGENE SA.
h 25.3%;
Similarity 33.4%;
                                                                                                                                                                                                                                                                                                                                                                                                   EOS BIOTECHNOLOGY IN 25.6%; Similarity 39.4%;
                                                                                                                                                                                                                                                                                                                                         RMF DICTAGENE SA.
                                                                                         COMPUGEN LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELI.
26.2%;
35.2%;
                                                                                                                                                                                                                                                                                                                     25.4%;
39.7%;
                                                                                                                                                     25.3%;
33.4%;
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35.2%;
                                                                     33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.9%;
38.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA1 protein sequence (Fig
25.1%;
                                                                     .24;
                                                                                                                       SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                        INC.
                                                                                                                                                                                                                                                                                                                                                                       1; 213 AA.
1 adhesion
                                                                                                                                                                                                                                                                                        ; 298 AA.
adhesion molecule 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222 AA.
) 6878.
                                                                                                                                  321
                                                                                                                                                                                                        adhesion
                                                                                                                                                                                                                  298 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 312
                                                                     Score
Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
 Score 387.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 402; DB 4;
Pred. No. 3.1e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
Pred.
                                                                                                                       21 AA.
) ID NO:129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₽
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                                                                      389;
No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    399
No.
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No. 2.
                                                                                                                                                                                                                                      391;
No. 1
                                                                                                                                                                                                                                                                                                                                                                                                     395
No.
                                                                                                                                                      391; DB 3;
No. 1.9e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404; DB 9;
No. 2.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       splice
                                                                                                                                                                                                                                                                                                                                                                       molecule
                                                                                                                                                                                                        molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.1e-21;
                                                                                                                                                                                                                                                                                                                                                                                                     5.9e-21;
                                                                      DB 5;
.8e-20;
                                                                                                                                                                                                                                                                                                                     ; DB 3;
.8e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 8;
.3e-21;
                                                                                                                                                                                                                                        9e B
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 BB
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                                                                                 321;
                                                                                                                                                                                                                                                 298;
 388;
                                                                                                                                                                                                                                                                                                                                 213;
                                                                                                                                                                                                                                                                                                                                                                                                                215;
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34.2%;

Pred.

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4.6e-20;

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Best Local Similarity
RESULT 1190
ID AAU18007 standard; F
DE Human immunoglobulin
PN W0200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME
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RESULT 1182
                                                                                                                                       Best Local Similarity RESULT 1189
                                                                                                                                                                                                                                                                                                                                      RESUL
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RESULT 1186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADF17957 standard; protein; 102 Averine junction adhesion molecule EP1318195-A1.
              Human immunoglobulin polypeptide WO200155315-A2.
                                                                                                                                                                                                                                                                                                                                                                                                    Cell adhesion and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADP56685 standard; prote Human junction adhesion WO2004053058-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human novel splice WO2003046180-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human protein EP1440981-A2.
                                                                                                        Novel human dia
WO200175067-A2.
                                                                                                                                                                                                                                                                                                      WO2003087128-A2.
                                                                                                                                                                                                                                                                                                                 Human adhesion molecule
                                                                                                                                                                                                                                                                                                                                                                                                             ADU06841 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUL-2004.
(REAS-) RES ASSOC BIOTECHNOLOGY.
22.8%; Score
20.8%; Pred.
                                                                                                                                                                                                      Human JAM-2 protein
WO2003104400-A2.
                                                                                                                                                                                                                                                                    (RMFD-) RMF DICTAGENE SA. (UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                                           WO2004094623-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADQ65675 standard;
                                                                                                                                               [RMFD-] RMF DICTAGENE SA.
(UYPE-) UNIV PENNSYLVANIA.
(YPE-) UNIV PENNSYLVANIA.
(YPE-) UNIV PENNSYLVANIA.
(UYPE-) UNIV PENNSYLVANIA.
(UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                            ADG39449 standard;
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                                                                                                                              NBG22401 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAO30179 standard;
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                                                                                   HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                           Match
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                                                                                                              andard; protein;
diagnostic prote
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                                                                                                                                                                                                                protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                 ELI.
21.1%;
32.9%;
                                                                                                                                                                                                                                                                                                                         protein;
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n sequence #648.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence
                                                                                                                                                                                                                                                21.0%;
33.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.1%;
38.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.8%;
                                                              20.4%;
                                                                                                                                                                                                                                                                                                                                               21.1%;
32.9%;
                                polypeptide
                                                                                                                  cein; 361 AA.
protein #22392.
                                                                                                                                                                                                                                                                                                                 ein; 238 AA.
JAM-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        molecule
                                                                                                                                                                                                                 ; 238 AA.
NO:18.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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e SEQ
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                                                              315;
                                                                                                                                                  325;
No.
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No.
                                                                                                                                                                                                                                                                                                                                               326.
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                   326
No.
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No.
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No.
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No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        splice
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                                Ħ
                                                                                                                                                                                                                                                                                                                                               8.5e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..5; DB 6;
5.9e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.2e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                   8.5
                                                                                                                                                 9.7e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                    protein clone 7518734CD1
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                                No 152
                                                                                                                                                                                                                                                                                                                                                                                                                                   ; DB 8;
                                                               DB 4;
                                                                                                                                                                                                                                                DB 7;
.7e-16;
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                                                                                                                                                             8,
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                                                                                                                                                             238;
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HUMAN GENOME SCI INC

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Best Local Similarity
RESULT 1191
ID AAM96332
                           Query Match
Best Local Similarity
RESULT 1199
                                                                                                        Best Loca.
RESULT 1198
                                                                                                                                                                                   Best Loca
RESULT 1197
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RESULT
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RESULT 1194
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Best Local Similarity
RESULT 1192
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RESULT 1193
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                                                                                                                                                                                                       Query Match
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Human NOV2a mature e
WO2004055158-A2.
01-JUL-2004.
                                                                          Mouse A33 antigen. WO9708189-A1.
                                                                                                                                                                                                                                   Human NOV2d protein WO2004055158-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB10436 standard;
Human cDNA SEQ ID
WO200154474-A2.
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Human junction adhesion WO2004053058-A2.
                  ADP56684 standard;
                                                                                                                                  01-JUL-2004.
(CURA-) CURAGEN CORP
                                                                                                                                                       Human NOV2c protein WO2004055158-A2
                                                                                                                                                                                                                                                                                                                                                                                              Human novel protein US2003077606-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP67023 standard;
Human polypeptide
US2002090672-A1.
                                                       06-MAR-1997.
(LUDW-) LUDWIG INST
                                                                                             AAW14158 standard;
                                                                                                                                                                          ADP69029 standard;
                                                                                                                                                                                                                        01-JUL-2004
                                                                                                                                                                                                                                                       ADP69031 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                 ADB31631 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                 (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                               (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME
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NO: 744.
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SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
system re
                                                                                                                                                                 protein; 206 AA.
n SEQ ID NO:24.
                                                                                                                                                                                                                                             protein; 206 AA.
n SEQ ID NO:26.
                                                                                                                                                                                                                                                                                                                                                                                                      protein; 105 AA.
1 SEQ ID NO 152.
                                    18.4%;
29.5%;
                                                                                               protein;
                                                                                                                                                                                                                                                                                                                           protein; 206 AA. extracellular do
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20.1%;
66.7%;
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20.1%;
66.7%;
                                                                                                                                                                                              19.8%;
34.0%;
                                                                                                                                                                                                                                                                          19.8%;
34.0%;
                                                                                                                                                                                                                                                                                                                                                       SCI INC
20.1%;
66.7%;
                                                                                                                34
                                                                                                                                                                                                                                                                                                                                                                                                                                     20.1%;
66.7%;
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66.7%;
          molecule
                                                                                                                                                                                                                                                                                                                                                                            INC.
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related a
                                    RES.
; Score
; Pred.
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Pred.
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Pred.
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Pred.
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                                                                                                                 305;
No. 2.
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No.
                                                                                                                                                                                                                                                                                                                                                                                                                                     310
No.
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No. 4.3e-15;
                                     284
No.
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No.
          aplice
                                      .5; DB 2;
1.3e-12;
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4.3e-15;
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4.3e-15;
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4.3e-15;
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                                                                                                                 DB 8;
.4e-14;
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.4e-14;
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.4e-14;
          variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ
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          (huJAM3sv1)
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                                                                                                                                                                                                                                                                                                                            NO:68
          protein.
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Best Local Similarity
RESULT 1200
ID ADK40854 star-
DE Human "
PN ""
Best Local Similarity
RESULT 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2004235768-A1.
25-NOV-2004.
(KORN/) KORNECKI E.
(SOBO/) SOBOCKA M B.
                                                                                                                                                                                                                                              AAB65863 standard;
Human A33 protein S
WO200078808-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG22338 standard; protein; Novel human diagnostic prote WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                           Human A33 antigen.
WO9708189-A1.
                                                                                                                                                                            ADA10947 standard; protein; 319 AA. Human cDNA differentially expressed
                                                                                                                                                                                                                                                                                                                              Amino acid sequence WO9927098-A2.
                                                                                                                                                                                                                                                                                                                                        AAY23323 standard; protein; 319 AA.
Amino acid sequence of the A33 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human A33 protein.
                                                                                       ADH62533 standard; protein; 319
Human A33 antigenic protein.
                                                                                                                                    )1-OCT-2002.
(LASE/) LASEK A W.
(JONE/) JONES D A.
                                                                                                                                                                    JS2002160382-A1.
                                                                                                                                                                                                         (MILL-) MILLENNIUM PHARM INC.
ry Match 17.6%;
L Local Similarity 25.8%;
                                                                                                                                                                                                                                                                                                                     03-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                             AAW14146 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                          GETH ) GENENTECH INC.
                                                          ASHK/) ASHKENAZI A
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1204
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                                                                               03171568-A1.
FONG S.
GODDARD A.
GURNEY A L.
NAPIER M A.
TUMAS D.
WOOD W I.
                                                                                                                                                                                                                                                         ; protein; 3
sEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELI.
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25.8%;
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33.3%;
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25.8%;
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18.1%;
26.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ein; 140 AA.
protein #22329
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; Score
; Pred. |
                                                                                                                                                                                                                                                           319
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Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                               319
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Pred.
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No. 2
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No.
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No. 9.5e-12;
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No. 1.3e-12;
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9.5e-12;
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Human A33 protein f
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                          Human polypeptide WO200218424-A2. 07-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                             AEB85134 standard; protein;
Human novel secreted protein
WO2005058028-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADP54587 standard; protein; 319 AA. Human PRO protein sequence SEQ ID NO:563 WO2004039956-A2.
                                                                                                                        ADH62553 standard; protein;
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                                                                                                    Human A33 antigenic US2003171568-A1.
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12-MAY-2003.
(EOSB-) EOS BIOTECHNOLOGY INC.
17.6%; Score
25.8%; Pred.
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) GENENTECH INC.
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                              ) GURNEY A L.
) NAPIER M A.
) TUMAS D.
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GODDARD A.
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                   WOOD W I.
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SEQ ID NO
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fragment #
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Pred. No. 9.5e-12;
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le-11;
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Best Local Similarity RESULT 1224
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RESULT 1222
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ID AAY08073
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Best Local Similarity
RESULT 1218
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                                                                                                                       Human signal peptide contain w0200000610-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                         ABM84859 standard; protein;
Human diagnostic and theraps
WO2004023973-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAO11807 standard;
Human polypeptide
WO200164835-A2.
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                                                                                                                                                                                                                                                                                                                          ABG12109 standard;
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(HYSE-) HYSEQ INC.
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An A33 related antigen sequence.
WO9927098-A2.
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Human A33 protein.
WO9914241-A2.
                   AAY94857 standard; protein; 327
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protein clone HP10568
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                                                       INCYTE PHARM INC.
15.0%;
Similarity 29.4%;
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diagnostic protein (
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                                                                                                                                                   rotein; 327 containing
                                                                                                                                                                                                            15.1%;
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86.
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US2003027988-A1.
ADB78209 standard; protein; Novel human secreted and traUS2003092886-Al.
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Human PRO polypeptide #118.
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Novel human secreted and transmembrane
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Human secreted/transmembrane
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Novel human secreted and transmembrane protein
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US2003069397-A1.
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ADC49702 standard; protein; 327 AA. Novel human secreted and transmembr US2003088071-A1.
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Human PRO polypeptide #118.
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Novel human secreted and transmembrane
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US2003100717-A1.
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Human PRO polypeptide #118.
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No. 9e-09;
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No. 9e-09;
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No. 9e-09;
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9e-09;
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9e-09;
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protein
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PR07154
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Best Local Similarity
RESULT 1307
ID ADM27354 standard; p
DE Novel human secreted
PN US2004044179-A1.
PD 04-MAR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1309
ID AAB5330
DE Human c
PN WO20005
PD 21-SEP-
PA (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                       RESULT
ID AF
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PD 05
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                                                                                                   Best Local Similarity RESULT 1314
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21-SEP-2000.
(HUMA-) HUMAN GENOME SCI INC.
15.0%;
15.0%;
27 Match 15.0%;
29.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human PRO polypeptide #118.
US2004044180-A1.
                                                           AAW31100 standard; peptide; 50 Platelet membrane glycoprotein US5665701-A. 09-SEP-1997.
                                                                                                                                                                                                                                                                                                                          ADF83097 standard; protein; 326 Human corticol thymocyte recepto WO2003100000-A2.
                                                                                                                                                                                                                                                                                                                                                                                                          AAG75613 standard; protein; 365 AA Human colon cancer antigen protein WO200122920-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADM27354 standard; protein; 327 AA. Novel human secreted and transmembr US2004044179-A1.
                                                                                                                                                                        ADU66687 standard;
Human FAM GluC-(4)
                                                                                                                                                                                                                                                       ADK40847 standard; peptide;
Human platelet F11-adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB53307 standard; protein;
Human colon cancer antigen |
WO200055351-A1.
AAB61480 standard;
Human CTH protein.
                            (UYNY ) UNIV NEW YORK STATE 
ry Match 14.7%; 
t Local Similarity 89.8%;
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15-APR-2001.

(HUWA-) HUMAN GENOME SCI INC.

15.0%;

ry Match 15.0%;

ry Match 29.4%;
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22-MAY-2003.
                                                                                                                                                    US2004235768-A1.
25-NOV-2004.
                                                                                                                                                                                                    .S6699688-b1.
J2-MAR-2004.
(UYNY ) UNIV NEW YORK STATE RES FOUND.
(UYNY ) T4.7%; Score 227;
                                                                                                                              (SOBO/) SOBOCKA M B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GETH ) GENENTECH INC
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                                                                                                                                                                                                                                                                                   Local Similarity
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peptide.
          protein;
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100.0%;
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28.8%;
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ı protein
                             RES FOUND.
Score 227;
Pred. No. 2
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                                                                                                                                                                                                                                                     42 AA.
molecule (FAM), peptide
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Pred.
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Pred.
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No.
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No. 1.5e-08;
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No. 1e-08;
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No. 1
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1e-08;
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9e-09;
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Best Local Similarity
RESULT 1322
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Best Local Similarity
RESULT 1320
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Best Local Similarity
RESULT 1316
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                                                                                                                                                                                                                                           ABU12083 standard; protein; 2572 AA. Human NOV25b CG93858-02 protein SEQ ID WO200281655-A2. 17-OCT-2002.
                                                                                  ADK60526 standard; protein; Angiogenesis differentially FR2836686-A1.
                                                                                                                                                                        ADK60225 standard; protein; Angiogenesis differentially FR2836687-A1.
                                                                                                                                                                                                                                                                                                                                        ADS98860 standard; protein; Protein factor discovery rel WO2004087874-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                  Human therapeutic WO2004080148-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                             T 1317
ADS10483 standard; protein;
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Protein similar to
US2003203843-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200100672-A1.
ADP73149 standard; protein; 2
Angiogenesis inhibitor human
FR2843753-A1.
                                                                                                                                                               05-SEP-2003
                                                       (GENE-) GENE SIGNAL. (ALMA/) AL MAHMOOD S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PENA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-JAN-2001
                                                                                                                                            (GENE-) GENE SIGNAL. (ALMA/) AL MAHMOOD S.
                                                                                                                                                                                                                                                                                                                                 14-OCT-2004.
                                                                                                                                                                                                                                                                                                                                                                                                (NUVE-) NUVELO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MILL-) MILLENNIUM
                                                                                                                                                                                                                                 (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                          (DRMA/) DRMANAC R T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EDIN,
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                                                                                                                         ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                           ocal Similarity
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PADIGARU M.
KEKUDA R.
SPYTEK K A.
SPYTEK K A.
TOPPER J N.
MALYANKAR U M.
WASSERMAN S M.
EDINGER S R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GUNTHER E.
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GUO X.
SHIMKETS
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                                     13.9%;
29.2%;
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29.2%;
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related
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expressed
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SEQ ID 720.
                  2673
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expressed
        2673 AA.
protein
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Pred.
                                     Score
Pred.
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Pred. No. 1.9e-06;
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Pred.
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Pred.
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Pred.
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Pred. No. 2.
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human
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                                      214
No.
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No. 1.9
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No. 1.2e-06;
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No. 1.9e-06;
          sequence,
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                                                                                              protein
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2e.
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           GS-P52
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Lest Local Similarity
RESULT 1324
                                                               Best Local Similarity RESULT 1327
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Best Local Similarity
RESULT 1326
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                                                                                                  Human FAM, Glu-C proteolytic US6699688-B1. 02-MAR-2004.
                                   ADU66696 standard; peptide; 42 AA.
Human FAM endoproteinase GluC proteolytic peptide.
US2004235768-A1.
                                                                                                                  ADK40856 standard; peptide; 42 AA.
Human FAM, Glu-C proteolytic fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADO08273 standard; protein;
Human NOVX polypeptide #10.
US2004018594-A1.
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(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human protein of the WO2003102155-A2.
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Human NOVX polypeptide #10.
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(ALMS/) AL M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-FEB-2004
                                                                      (UYNY ) UNIV NEW YORK STATE

TY Match 13.9%;
Local Similarity 97.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADH72106 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-NOV-2002.
(CURA-) CURAGEN CORP.
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Match
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RIEGER D K.
SHINKETS R A.
SPYTEK K A.
TAUDIER R J.
VERNET C A M.
VOSS E Z.
ZERHUSEN B D.
                                                                                                                                                                                                                                                                                                                               CASMAN S J.
CHAPOVAL A.
EDINGER S R.
GERLACH V.
GORMAN L.
GUNTHER E.
GUO X S.
                                                                                                                                                                                                                                                                                                                                                                                              ANDERSON D W.
BOLDOG F L.
BURGESS C E.
        KORNECKI E.
                                                                                                                                                                                                                                                 PADIGARU M.
PATTURAJAN M.
                                                                                                                                                                                                                                                                   MILLER C E.
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LEPLEY D M.
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Score 214;
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Score 214;
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42;
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RESULT
ID AB
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RESULT
                                                  Best Local Similarity RESULT 1333
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Best Local Similarity
RESULT 1331
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                                                                                              Human NOV25c CG56914-03 protein SEQ MO200281625-A2.
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                                                                                                                                                                                                                                                                                                                                  Protein similar
US2003203843-A1.
                  ADH72108 standard; protein; 1902 AA. Human protein of the invention NOV43d SEQ ID NO:1004. WO2003102155-A2.
                                                                                                                                                                                                                                    (PENA/)
(GUOX/)
(SHIM/)
(PADI/)
(PADI/)
(KEKU/)
(KEYT/)
(MEHR/)
                                                                                                                                                                                                                                                                                                                                            ADG39840 standard; protein; 1708 AA. Protein similar to human NOV9 #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein similar
US2003203843-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADG39841 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FARB ) BAYER CORP.
                                                                                 17-OCT-2002.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                           (EDIN,
                                                                                                                                                                                                                                                                                                                                                                                                                       TIMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GUOX/)
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                                                                                                                                                                                                                (WASS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KEKU/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PENA/)
(CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                   GUNTHER E. KOMUVES L.
                                                                                                                                                                                                                                                                                                                                                                                              SMITHSON G.
GUNTHER E.
KOMUVES L.
                                                                                                                                                                                        KEKUDA R.
SPYTEK K A.
MEHRABAN F.
TOPPER J N.
MALYANKAR U I
WASSERWAN S I
EDINGER S R.
SMITHSON G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GUO X.
SHIMKETS
PADIGARU
                                                                                                                                                                                                                                                                            SHIMKETS R F
PADIGARU M.
                                                                                                                                                                                                                                                                                                                                                                                                                               MALYANKAR U I
WASSERMAN S I
EDINGER S R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEKUDA R.
SPYTEK K A.
MEHRABAN F.
TOPPER J N.
                                                                                                                                                                                                                                                                                                              PENA C E A.
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29.2%;
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29.2%;
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29.2%;
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29.2%;
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29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1708 AA.
V9 #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
Pred.
                                                                                                                                                Score
Pred.
                                                             Score 213.5; DB 6
Pred. No. 1.6e-06;
                                                                                                                                                                                                                                                                                                                                                                           Score 213.5; DB 7;
Pred. No. 1.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 213.5; DB 4
Pred. No. 9.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213
No.
                                                                                                                                                213.5; DB 7
No. 1.4e-06;
                                                                                                                 IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.5; DB 5
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                                                                                                                                                          DB 7;
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                                                                       Length 1902;
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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                             G-coupled protein WO200283841-A2.
                                                                                                                                                                                                                                                                                                                                                                           ADL93997 standard;
Human G-coupled pro
US2004006205-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADE16058 standard;
                                                                                                                                                          Human hemicentrin
US2003170630-A1.
                                                             (CASM/)
                                                                          (VERN,
                                                                                                                                                                      ADJ83136 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                 CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                           PENA
                                                                                                                                                                                                                                                                                                                                                         GERL/) GERLACH V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                  Local Similarity
                 CASMAN S J.
BOLDOG F L.
GORMAN L.
GANGOLLI E A.
FERNANDES E R.
RIEGER D K.
EDINGER S R.
EDINGER S R.
                                                                        SPYTEK K A.
ZERHUSEN B D.
PATTURAJAN M.
LEPLEY D M.
BURGESS C E.
SHIMKETS R A.
GROSSE W M.
SZEKERES E S.
VERNET C A M.
                                                                                                                                                                                                                       PATTURAJAN M.
BURGESS C E.
MALYANKAR U M.
                                                                                                                                                                                                                                                                               SMITHSON G.
CASMAN S J.
BOLDOG F L.
VOSS E Z.
VERNET C A.
                                                                                                                                                                                                     SHIMKETS R A. TAUPIER R J. EDINGER S.
                                                                                                                                                                                                                                                            MACDOUGALL J R.
RASTELLI L.
ANDERSON D W.
                                                                                                                                                                                                                                               ZHONG M.
MEZES P S.
                                                                                                                                                                                                                                                                                                                    MILLER C
SPYTEK K
ZERHUSEN
PENA C E
SHENOY S
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                                                                                                                                       ALSOBROOK J P.
TCHERNEV V T.
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                                                                                                                                                                                                                                                                                                                                                                                  protein
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                                                                                                                                                               ; protein;
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                                                                                                                                                                                                                                                                                                                                                                                        protein; 1953
                                                                                                                                                                                                                                                                                                                                                                                                                                          protein;
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29.2%;
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29
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                                                                                                                                                                                                                                                                                                                                                                                                     8#;
                                                                                                                                                                                                                                                                                                                                                                                  receptor-related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 1953 AA.
related p
                                                                                                                                                                3645 AA.
SEQ ID 127
                                                                                                                                                                                  Pred. No. 1.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                     Score
Pred.
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Pred. No. 1.6
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No.
                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide,
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                                                                                                                                                                                        Length 1953;
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Query Match
Best Local Similarity
RESULT 1337
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DE CONTROL DID
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Best Local Similarity
RESULT 1341
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RESULT 1338
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Query Match
Best Local Similarity
                                                                                              ADK60205 standard; protein; Angiogenesis differentially FR2836687-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human hemicentin US2003170630-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADJ70089 standard; protein; 5636 AA. Human heat mitochondrial protein as a therapeutic WO2003087768-A2.
23-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP60991 standard; protein; Novel human protein. SEQ ID WO200250105-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEB94406 standard; protein;
Human hemicentin/FIBL-6 prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADJ83137 standard,
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(VERN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE B
(SMIK ) SMITHKLINE B
(GLAX ) GLAXO GROUP
                          (GENE-) GENE SIGNAL
                                                                                                                                                                                                                                                           (SCIO/)
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(SMIT/) SMITHSON G.
                                                                                                                                                                                                                      (SMIT/)
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                                GENE SIGNAL.
                                                                                                                                                                                                                                                                                                                                   CASMAN S J.
BOLDOG F L.
GORMAN L.
GANGOLLI E A.
FERNANDES E R.
RIEGER D K.
EDINGER S R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPYTEK K A.
ZERHUSEN B D.
PATTURAJAN M.
LEPLEY D M.
BURGESS C E.
SHIMKETS R A.
GROSSE W M.
SZEKERES B S.
VERNET C A M.
                                                                                                                                                                                                                                                        MILLET I.
SCIORE P.
ELLERMAN K.
                                                                                                                                                                                                                                                                                                                  EDINGER S I
                                                                                                                                                                                                                 MACDOUGALL
SMITHSON G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIT
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29.2%;
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29.2%;
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29.2%;
29.
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protein, SEQ
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SEQ ID 128.
                                                                                                                   5636 AA.
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78.
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Pred.
Score
Pred.
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Pred.
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Pred.
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Pred.
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213
No.
                                                                                                                                                                              No. 5.6
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No.
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No. 5.6e-06;
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                                                                                                                     protein GS-P29
  .5; DB 8;
5.6e-06;
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.6e-06;
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e-06;
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                  Length
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RESULT 1342

ID ADK60506 standard; protein; 5

DE Angiogenesis differentially e
PN FR2836686-A1.
PD 05-SEP-2003.
PA (GEME-) GEME SIGNAL.
PA (ALMA/) AL MAHMOOD S.
                     Best Local Similarity RESULT 1350
                                                                                                           Best Local
RESULT 1349
                                                                                                                                                                                                Best Local Similarity RESULT 1348
                                                                                                                                                                                                                               Best Local Similarity
RESULT 1345
                                                                                                                                                                                                                                                                                                         RESULT 1347
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                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
 AAB08940 standard; protein; 245 AA.
Human secreted protein sequence encoded
                                                                           Human novel protein US2003077606-A1.
                                                                                                                                                               Human immunoglobulin WO200155315-A2.
                                                                                                                                                                                     AAU18038 standard;
                                                                                                                                                                                                                                                                        Human hemicentin
US2005164277-A1.
                                                                                                                                                                                                                                                                                                                                                             Human hemicentin
US6867291-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2005164277-A1.
28-JUL-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEB34668 standard; protein; 4126 AA.
Human hemicentin protein, SEQ ID 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADY74314 standard;
Human hemicentin p
US6867291-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADP73129 standard; protein; 5636 AA. Angiogenesis inhibitor human protein FR2843753-A1.
                                (HUMA-) HUMAN GENOME SCI INC.
ry Match 13.6%;
t Local Similarity 26.3%;
                                                                                                ADB31662 standard;
                                                                                                                                                                                                                                                                                  AEB34666 standard; protein;
Human hemicentin protein, SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENE/) GENE S. (ALMS/) AL M S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENE-) GENE SIGNAL (ALMA/) AL MAHMOOD
                                                                                                                    (HUMA-) HUMAN GENOME SCI INC. ry Match 13.6%; Local Similarity 26.3%;
                                                                                                                                                                                                                                                                                                                                                                                     ADY74312 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                            (TURN/) TURNER C
(MATH/) MATHUR B.
(DONO/) DONOHO G.
                                                                                                                                                                                                                                                                                                                                        LEXI-) LEXICON GENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEXI-) LEXICON GENETICS INC.
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                                                                                                                                                                                                                                                                                                                                 Match
                                                                                                                                                                                                                                                                                                                   ocal Similarity
                                                                                                                                                                                                                             ) TURNER C A.
) MATHUR B.
) DONOHO G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₽
                                                                                                                                                                                                                                                                                                                                                                        i; protein; protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; protein; 4126
protein lacking
                                                                                     protein; 294 AA
n SEQ ID NO 183.
                                                                                                                                                                         protein; 294 AA.
in polypeptide SEQ
                                                                                                                                                                                                                                                                                                                   13.8%;
29.2%;
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29.2%;
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29.2%;
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29
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29
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SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5636 AA.
expressed
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                                 Score
Pred.
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Pred.
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Pred.
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Pred. No. 5.6
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part
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No. 3.
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No.
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No. 6.5
                                210;
No. 3.
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No.
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Best Local Similarity RESULT 1356
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RESULT 1355
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WO200200690-A2.
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Human secreted protein sequence encoded
WO20001722-A1.
30-MAR-2000.
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Human PRO5723 protein.
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WO200116319-A2.
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30-MAR-2000.
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Human PRO5723 protein.
US2002192752-A1.
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Human PRO polypeptide #108.
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Human PRO5723 polypeptide.
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US2002123463-A1.
05-SEP-2002.
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US2003027985-A1.
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US2002197615-A1.
26-DEC-2002.
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       Human PRO5723 protein.
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                      ABJ72463 standard;
                                                            Human secreted/transmembrane US2003059780-A1.
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Human PRO5723 poly;
US2003054987-A1.
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US2003065147-A1.
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22-MAY-2003.
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US2003045463-A1.
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ADC49682 standard;
Novel human secrete
US2003088071-A1.
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Novel human secrete
US2003088064-A1.
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RESULT 1416
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Human PRO polypeptide #141.
US2003059833-A1.
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Human PRO polypeptide #141.
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Novel human secreted and transmembrane protein
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Human secreted/transmembrane
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rRO polypeptide #141.
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Novel human secreted and transme
US2002193300-A1.
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                                                                                    ADD51126 standard; protein; Novel human secreted and traUS2003105290-A1.
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Human secreted/transmembrane
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Query Match
Best Local Similarity
RESULT 1438
ID ADD54874 standard; p
DE Human PRO polypeptid
PN US2002132253-A1.
PD 19-SEP-2002
PA (GETH ) GENENTECH IN
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ID ADD5137:
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PN US20031(
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Human secreted/transmembrane
US2003105012-A1.
                                                             ADE26495 standard; protein; 352 AA Novel human secreted and transmemb
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Novel human secreted and transmembrane
US2003105289-A1.
05-UUN-2003.
(GETH ) GENENTECH INC.
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Human PRO polypeptide #141.
US2002132253-A1.
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                                         US2003087305-A1.
08-MAY-2003.
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Human PRO polypeptide #108.
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  ADF67432
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Best Local Similarity
RESULT 1445
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DE Immune disease treat
PN US2003082199-A1.
PD 01-MAY-2003
PA (GETH) GENENTECH IN
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RESULT 1448
ID ADC4891
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PN US20030
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US200310075-A1.
29-MAY-2007
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US2003050457-A1.
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ADD85141 standard; protein; 352 AA. Novel human secreted and transmembr US2003100722-A1.
29-MAY-2003.
                                                                                                        ADD75909 standard; protein; 352 AA. Novel human secreted and transmembrane
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15-MAY-2003.
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26-DEC-2002.
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Novel human secreted and transmembrane
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RESULT 1462
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RESULT 1458
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Human PRO polypeptide #108.
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Human PRO polypeptide #108.
US2003100727-Al.
29-MAY-2003.
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Novel human secreted and transmembrane protein PRO5723
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Novel human secreto
US2003100734-A1.
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US2003100733-A1.
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                  ADD76953 standard; protein; 352 Novel human secreted and transme US2003100715-A1.
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Human PRO polypeptide #108.
US2003100726-A1.
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Best Local Similarity
RESULT 1476
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PD 29-MAY-2003.
PA (GETH) GENENTECH INC
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Human PRO polypeptide #108.
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22-MAY-2003.
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Query Match
Best Local Similarity 26.7%; Pred. No.
RESULT 1499
ID ADI29937 standard; protein; 352 AA.
DE Novel human secreted and transmembrane
PN US2003096961-A1.
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(GETH ) 13.4%; (
March 13.4%; (
                                         US2004-2004.
29-JAN-2004.
(GETH) GENENTECH INC.
13.4%; !
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Human PRO polypeptide #140.
US2003324984-A1.
04-DEC-2003.
(GETH) GENENTECH INC.
                                                                                                                                                                                           Human PRO polypeptide #108.
US2003096960-A1.
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Novel human secreted and transmembrane protein

US2003096965-A1.

22-MAY-2003.

(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                         ADG34212 standard; protein; 352 AA. Novel human secreted and transmembrane US2004006206-A1. 08-JAN-2004. (GETH ) GENENTECH INC.
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Human PRO polypeptide #108.
US2004019183-A1.
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27-NOV-2003.
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PD 22-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match

Best Local Similarity 26.7%; Pred. No. 6.1e-07;

RESULT 1500

ID ADM27334 standard; protein; 352 AA.

DE Novel human secreted and transmembrane protein PRO5723.

PN US200404179-A1.

PD 04-MAR-2004.

PA (GETH) GENENTECH INC.

13.4%; Score 207.5; DB 8; Length 352;

Best Local Similarity 26.7%; Pred. No. 6.1e-07;
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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RESULT 2 US-09-462-270-2 i Sequence 2, Application US/09462270 patent No. 6358707 patent No. 6358707 patent SmithKline Beecham Corporation papelicant: SmithKline Beecham Corporation papelicant SmithKline Beecham Corporation papelicant SmithKline Beecham Corporation papelicant SmithKline Beecham Corporation		61 EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYG	Query Match  100.0%; Score 1544; DB 2; Length 299;  Best Local Similarity 100.0%; Pred. No. 8.3e-135;  Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy 1 MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV 60	APPLICANT: Watson, James D.  APPLICANT: Strachan, Lorna APPLICANT: Sleeman, Matthew APPLICANT: Orrust, Rene APPLICANT: Murison, James Greg TITLE OF INVENTION: Compositions Isolated From Skin Cells TITLE OF INVENTION: and Methods For Their Use FILE REFERENCE: 11000.1011c1 CURRENT APPLICATION NUMBER: US/9/188,930A CURRENT FILING DATE: 1998-11-09 NUMBER OF SEQ ID NOS: 348 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 331 LENGTH: 299 TYPE: PRT ORGANISM: Human US-09-188-930-331	RESULT 1 US-09-188-930-331 ; Sequence 331, Application US/09188930A ; Patent NO. 6150502 ; GENERAL INFORMATION:	1488 94.5 6.1 270 2 US-09-976-118-2 Sequence 2, Appli 1489 94.5 6.1 313 2 US-09-756-983-15 Sequence 15, Appl 1490 94.5 6.1 360 2 US-09-949-016-8370 Sequence 8370, Appli 1491 94.5 6.1 432 2 US-08-477-460B-2 Sequence 2, Appli 1492 94.5 6.1 432 2 US-08-379-516-2 Sequence 2, Appli 1493 94.5 6.1 432 2 US-09-329-916-2 Sequence 2, Appli 1494 94.5 6.1 432 2 US-09-329-916-2 Sequence 2, Appli 1495 94.5 6.1 432 2 US-09-409-006A-2 Sequence 2, Appli 1496 94.5 6.1 432 2 US-09-409-006A-2 Sequence 2, Appli 1497 94.5 6.1 432 2 US-08-484-681-2 Sequence 2, Appli 1498 94.5 6.1 432 2 US-08-484-681-2 Sequence 2, Appli 1499 94.5 6.1 432 2 US-08-484-681-2 Sequence 2, Appli 1499 94.5 6.1 432 2 US-08-76-995-2 Sequence 2, Appli 1499 94.5 6.1 432 4 PCT-US93-0742-2 Sequence 2, Appli 1499 94.5 6.1 432 4 PCT-US93-0742-2 Sequence 2, Appli 1499 94.5 6.1 432 4 PCT-US93-0742-2 Sequence 2, Appli 1499 94.5 6.1 432 4 PCT-US93-0742-2 Sequence 2, Appli 1499 94.5 6.1 432 4 PCT-US93-0742-2 Sequence 2, Appli 1499 94.5 6.1 432 4 PCT-US93-0742-2 Sequence 2, Appli 1499 94.5 6.1 432 4 PCT-US93-0742-2 Sequence 2, Appli 1499 94.5 6.1 432 4 PCT-US93-0742-2 Sequence 2, Appli 1499 94.5 6.1 432 4 PCT-US93-0742-2 Sequence 2, Appli 1499 94.5 6.1 432 4 PCT-US93-0742-2 Sequence 2, Appli 1499 94.5 6.1 432 4 PCT-US93-0742-2 Sequence 2, Appli 1499 94.5 6.1 432 4 PCT-US93-0742-2 Sequence 2, Appli 1499 94.5 6.1 432 4 PCT-US93-0742-2 Sequence 2, Appli 1499 94.5 6.1 432 4 PCT-US93-0742-2 Sequence 2, Appli 1499 94.5 6.1 432 4 PCT-US93-0742-2 Sequence 2, Appli 1499 94.5 6.1 432 4 PCT-US93-0742-2 Sequence 2, Appli 1499 94.5 6.1 432 4 PCT-US93-0742-2 Sequence 2, Appli 1499 94.5 6.1 432 4 PCT-US93-074-81 Sequence 2, Appli 1499 94.5 6.1 432 4 PCT-US93-074-81 Sequence 2, Appli 1499 94.5 6.1 432 4 PCT-US93-074-81 Sequence 2, Appli 1499 94.5 6.1 432 4 PCT-US93-074-81 Sequence 2, Appli 1499 94.5 6.1 432 4 PCT-US93-074-81 Sequence 2, Appli 1499 94.5 6.1 432 4 PCT-US93-074-81 Sequence 2, Appli 1499 94.5 6.1 432 4 PCT-US93-074-81 Sequence 2, Appli 1499 94.5 6.1 432 4 PCT-US93-074-81 Seq

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FILE OF INVENTION: Receptor Involved in FILE REFERENCE: GH-70150US CURRENT APPLICATION NUMBER: US/09/462,270 CURRENT FILING DATE: 2000-01-05 PRIOR APPLICATION NUMBER: 60/052,186 PRIOR FILING DATE: 1997-07-10 NUMBER OF SEQ ID NOS: TO SEQ ID NOS: T
                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/254,465A
CURRENT FILING DATE: 1999-03-05
PRIOR APPLICATION NUMBER: PCT/US98/24855
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: US 60/066,364
PRIOR APPLICATION NUMBER: US 60/078,936
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 60/078,936
PRIOR FILING DATE: 1998-03-20
PRIOR PRIOR APPLICATION NUMBER: PCT/US98/19437
PRIOR APPLICATION NUMBER: PCT/US98/19437
PRIOR PILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 1
LENGTH: 299
TYPES: DET
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US-09-254-465A-1
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   Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Genentech, Inc.
APPLICANT: Ashkenari, Avi J.
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Napier, Mary A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
TILE REFERENCE: P1216R1(US)
                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
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Pred. No. 8.3e-135;
); Mismatches 0;
       Score 1544;
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US-09-312-283C-189
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APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from TITLE OF INVENTION: and Methods for Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 199-05-14
NUMBER OF SEQ ID NOS: 425
SOFTMARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 189
LENGTH: 299
TYPE: PRT
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Patent No. 6573095
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                   AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV
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APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Steman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 199-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 331
LENGTH: 299
TYPE: PRT
ORGANISM: Mouse
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US-09-907-794A-119
; Sequence 119, Application US/09907794A
; Patent No. 663546B
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                                                                                                                                                                                                     Genntech, Inc.
Ashkenazi, Avi
Becstein, David
Desnoyers, Luc
Eston, Dan L.
Eston, Dan L.
Ferrara, Napoleone
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Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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                                                                         Godowski, Paul J.
Grimaldi, Christopher
                                                                                                                               Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                  Goddard, A.
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FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR PPLICATION NUMBER: US 60/143,048
PRIOR PPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR PPLICATION NUMBER: PCT/US99/2054
PRIOR APPLICATION NUMBER: PCT/US99/2199
PRIOR APPLICATION NUMBER: PCT/US99/2199
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21647
PRIOR APPLICATION NUMBER: PCT/US99/21647
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR PILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR PILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28564
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PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 119
SEQ ID NO 119
LENGTH: 299
TYPE: PRT
ORGANISM: Homo sapiens
US-09-907-794A-119
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PRIOR APPLICATION NUMBER: PCT/US99/28564

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR APPLICATION NUMBER: PCT/US99/30911

PRIOR APPLICATION NUMBER: PCT/US99/30911

PRIOR APPLICATION NUMBER: PCT/US99/30911

PRIOR FILING DATE: 1999-12-20

PRIOR FILING DATE: 1999-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 299; Conservative 0
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APPLICANT:
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
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APPLICATION NUMBER: PCT
FILING DATE: 1999-12-20
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Stewart, Timothy A.
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Pred. No. 8.3e-135;
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US-09-905-125A-119
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CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
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APPLICANT: Genentech, Inc.
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              OR FILING DATE: 1999-11-29
OR FILING DATE: 1999-11-29
OR APPLICATION NUMBER: PCT/US99/28313
OR APPLICATION NUMBER: PCT/US99/28564
OR APPLICATION NUMBER: PCT/US99/28565
OR APPLICATION NUMBER: PCT/US99/30095
OR APPLICATION NUMBER: PCT/US99/30095
OR FILING DATE: 1999-12-16
OR APPLICATION NUMBER: PCT/US99/30911
OR APPLICATION NUMBER: PCT/US99/30999
OR FILING DATE: 1999-12-20
OR FILING DATE: 1999-12-20
OR FILING DATE: 1999-12-20
                                                                                                                                                                                                                                                                                                                             OR APPLICATION NUMBER: PCT/US99/20944
OR FILING DATE: 1999-09-13
OR APPLICATION NUMBER: PCT/US99/21090
OR FILING DATE: 1999-09-15
OR APPLICATION NUMBER: PCT/US99/21547
OR FILING DATE: 1999-09-15
OR FILING DATE: 1999-09-15
OR APPLICATION NUMBER: PCT/US99/23089
OR APPLICATION NUMBER: PCT/US99/28214
APPLICATION NUMBER: PCT/US00/00219
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Wood, William,
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Mather, Jennie P.
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Grimaldi, Christopher
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Botstein, David
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Filvaroff, Ellen
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US-09-905-125A-119
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; SEQ ID NO 119
; LENGTH: 299
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Best Local Sim
Matches 299;
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                                                                                         APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and :
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
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PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
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Mather, Jennie P.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Grimaldi, Christopher
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Filvaroff, Ellen
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Ashkenazi, Avi
Botstein, David
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GENERAL INFORMATION:
APPLICANT: Kornecki, Blizabeth
APPLICANT: Sobocka, Malgorzata B.
TITLE OF INVENTION: Human Platelet F11 Receptor
FILE REFERENCE: 011.00221
CURRENT APPLICATION NUMBER: US/09/397,243D
CURRENT FILING DATE: 1999-09-16
PRIOR APPLICATION NUMBER: 60/100,638
PRIOR FILING DATE: 1998-09-16
                                                                                                                                                          Sequence 3, Application US/09397243D Patent No. 6699688
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Best Local
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ORGANISM: Homo sapiens
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OR PILING DATE: 1999-10-05
OR APPLICATION NUMBER: PCT/US99/28214
OR FILING DATE: 1999-11-29
OR APPLICATION NUMBER: PCT/US99/28313
OR FILING DATE: 1999-11-30
OR APPLICATION NUMBER: PCT/US99/28564
OR FILING DATE: 1999-12-02
OR APPLICATION NUMBER: PCT/US99/28565
OR APPLICATION NUMBER: PCT/US99/28565
OR APPLICATION NUMBER: PCT/US99/30095
OR APPLICATION NUMBER: PCT/US99/30095
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FILING DATE: 1999-12-20
APPLICATION NUMBER: PCT/US00/00219
FILING DATE: 2000-01-05
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APPLICATION NUMBER: PCT/US99/30911
FILING DATE: 1999-12-20
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FILING DATE: 1999-09-13
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Similarity 100.0%;
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Pred. No. 8.3e-135;
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RESULT 10
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; ORGANISM: Homo sapiens
US-09-397-243D-3
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SEQ ID NO 3
LENGTH: 299
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APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 672353
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Best Local Similarity
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           APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION UNMBER: US/09/906,700
CURRENT FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
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APPLICATION NUMBER:
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Eaton, Dan L.
Ferrara, Napoleone
Ferraraff, Ellen
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Stewart, Timothy A.
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Grimaldi, Christopher
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US 60/145,698
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Pred. No. 8.3e-135;
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DATE: 1999-07-26

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PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR PELLING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR PELLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 119
LENGTH: 299
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US-09-903-603A-119
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APPLICANT: Genentech, I
APPLICANT: Ashkenazi,
APPLICANT: Botatein, I
APPLICANT: Desnoyers,
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Na
APPLICANT: Filvaroff,
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GENERAL INFORMATION:
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OR FILING DATE: 1999-07-28

FOR APPLICATION NUMBER: PCT/US99/20594

OR APPLICATION NUMBER: PCT/US99/20944

OR APPLICATION NUMBER: PCT/US99/20944

OR APPLICATION NUMBER: PCT/US99/21090

OR FILING DATE: 1999-09-15

OR APPLICATION NUMBER: PCT/US99/21547

OR APPLICATION NUMBER: PCT/US99/23089

OR FILING DATE: 1999-10-05

OR FILING DATE: 1999-10-05

OR APPLICATION NUMBER: PCT/US99/28214

OR APPLICATION NUMBER: PCT/US99/28313

OR APPLICATION NUMBER: PCT/US99/28313

OR APPLICATION NUMBER: PCT/US99/28564

OR APPLICATION NUMBER: PCT/US99/28565

OR FILING DATE: 1999-12-16

OR APPLICATION NUMBER: PCT/US99/28565

OR APPLICATION NUMBER: PCT/US99/30095

OR FILING DATE: 1999-12-16
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                                         Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L
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Ferrara, Napoleone
Filvaroff, Ellen
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                                                                                                                                  ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-903-603A-119
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PRIOR FILING DATE: 1
PRIOR APPLICATION NU
PRIOR FILING DATE: 2
NUMBER OF SEQ ID NOS
SEQ ID NO 119
LENGTH: 299
                                                       Query Match
Best Local Similarity
Matches 299; Conserv
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: GNE.1618P2C12
CURRENT APPLICATION NUMBER: US/09/903,603A
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1090-07-07
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
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APPLICANT:
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PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US99/30999
FILING DATE: 1999-12-20
APPLICATION NUMBER: PCT/US00/00219
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FILING DATE: 1999-09-08
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FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
FILING DATE: 1999-10-05
                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US99/30095 FILING DATE: 1999-12-16
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APPLICATION NUMBER: PCT/US99/28564
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APPLICATION NUMBER: PCT/US99/28313
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                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1999-12-02
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APPLICATION NUMBER: PCT/US99/28565
MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRI PENNPVKLSCAYSGFSSPRV
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Mather, Jennie P.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Grimaldi, Christopher J.
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                                                           Conservative
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art, Timothy A.
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                                                                         100.0%;
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Pred. No. 8.3e-135;
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APPLICANT: William, P. Mickey
APPLICANT: Wood, William, I.
FITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,920A
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US/09/904,920A
CURRENT FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/23089
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                OR FILING DATE: 1999-09-15
OR APPLICATION NUMBER: PCT/US99/21547
OR FILING DATE: 1999-09-15
OR APPLICATION NUMBER: PCT/US99/23089
OR FILING DATE: 1999-10-05
OR PILICATION NUMBER: PCT/US99/28214
OR FILING DATE: 1999-11-29
OR APPLICATION NUMBER: PCT/US99/28313
FILING DATE:
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Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
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Stewart, Timothy A.
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Filvaroff,
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Botstein, David
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Mather, Jennie P.
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f, Ellen
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PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR FPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR FPLICATION NUMBER: PCT/US00/00219
PRIOR FPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-920A-119
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Best Local Similarity
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FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/28565
FILING DATE: 1999-12-02
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                                  AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV 299
                                                                          RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV
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Pred. No. 8.3e-135;
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RESULT 13 US-09-909-064-119 GENERAL INFO Sequence 119, Application US/09909064 Patent No. 6818449 APPLICANT: APPLICANT APPLICANT APPLICANT APPLICANT INFORMATION: Genentech, Gurney, Austin L. Hillan, Kenneth, J. Kljavin, Ivar J. Mather, Jennie P. Stewart, Timo Tumas, Daniel Roy, Margaret Ann crewart, Timothy A. Godowski, Paul J. Grimaldi, Christopher Gerber, Hanspeter Gerritsen, Mary E Gao, Ferrara, Napoleone Filvaroff, Ellen Desnoyers, Luc Eaton, Dan L. Ashkenazi, Avi Botstein, David Williams, Paoni, Pan, Goddard, Fong, James Wei-Qiang Sherman Nicholas F. , A. Inc. P. Mickey 4

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-064-119
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SEQ ID NO 119
LENGTH: 299
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PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR TILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
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PRIOR TILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
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PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-20
PRIOR APPLICATION NUMBER: PCT/US99/28313
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PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
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PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
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CURRENT FILING DATE: 2001-07-18
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APPLICATION NUMBER: PCT/US99/30095
FILING DATE: 1999-12-16
APPLICATION NUMBER: PCT/US99/30911
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APPLICATION NUMBER: PCT/US99/28565
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AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV 299
                              AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV 299
                                                                                             RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV
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RESULT 14

ORGANISM: Homo sapiens

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PRIOR FILING DATE:
NUMBER OF SEQ ID NO.
SEQ ID NO. 119
LENGTH: 299
TYPE: PRT
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PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
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GENERAL INFORMATION:
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,381A
CURRENT FILING DATE: 2001-07-13
                                                                               PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
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PRIOR APPLICATION NUMBER: PCT/US99/20944
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APPLICANT: Ashkenazi
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FILING DATE: 1999-11-30
APPLICATION NUMBER: PCT/US99/28564
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                                                                                                                                                                                 FILING DATE: 1999-12-16
APPLICATION NUMBER: PCT/US99/30911
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Mather, Jennie P.
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Hillan, Kenneth, J.
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Grimaldi, Christopher
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Gerritsen, Mary E
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Filvaroff, Ellen
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Botstein, David
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art, Timothy A.
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CURRENT APPLICATION NUMBER: US/09/906,618
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR PRIOR DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-8
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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APPLICATION NUMBER: PCT/US99/20944
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Roy, Margaret Ann
Stewart, Timothy A.
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Botstein, David
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Grimaldi, Christopher
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Mather, Jennie P.
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Hillan, Kenneth, J.
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Filvaroff, Ellen
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Pred. No. 8.3e-135;
Mismatches 0;
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LENGTH: 299
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PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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OR FILING DATE: 1999-12-16
OR APPLICATION NUMBER: PCT/US99/30911
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FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
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